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OM protein - protein search, using sw model

Run on: November 17, 2004, 15:29:03 ; Search time 162 Seconds

(without alignments)
460.91 Million cell updates/sec

Title: US-10-019-065A-1

Perfect score: 1231

Sequence: 1 QVHGGFQSOWSAWCACSVTCG.....SCGGGARQRTGCGCSDPVPQY 208

Scoring table: BL0SUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23Seq04;*

1: geneseqP1980;*

2: geneseqP1990;*

3: geneseqP2005;*

4: geneseqP20018;*

5: geneseqP20028;*

6: geneseqP2003as;*

7: geneseqP2003bs;*

8: geneseqP2004as;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1231	100.0	208	5 AAB47770	Aab47770 Human thr
2	1231	100.0	707	6 ABU69134	Abu69134 Human NOV
3	1231	100.0	707	8 ADH672102	Adh672102 Human PRO
4	1231	100.0	707	8 AD008271	Ado08271 Human NOV
5	1231	100.0	1336	5 AAB47771	Aab47771 Human thr
6	1231	100.0	1708	7 ADG39841	Adg39841 Protein S
7	1231	100.0	1708	7 ADG39840	Adg39840 Protein S
8	1231	100.0	1902	6 ABU12054	Abu12054 Human NOV
9	1231	100.0	1902	8 ADH72108	Adh72108 Human PRO
10	1231	100.0	5635	5 ABP60991	Abp60991 Novel hum
11	1231	100.0	5636	7 ADJ70089	Adj70089 Human hea
12	1231	100.0	5636	7 ADJ83137	Adj83137 Human hem
13	1231	100.0	5636	8 ADK60205	Adk60205 Angiogene
14	1231	100.0	5636	8 ADK60506	Adk60506 Angiogene
15	1231	100.0	5636	8 ADP73129	Adp73129 Angiogene
16	1230	99.9	1708	7 ADG39844	Adg39844 Protein S
17	1230	99.9	2572	6 ABU12083	Abu12083 Human NOV
18	1230	99.9	2673	8 ADK60225	Adk60225 Angiogene
19	1230	99.9	2673	8 ADK60526	Adk60526 Angiogene
20	1230	99.9	2673	8 ADP73149	Adp73149 Angiogene
21	1230	99.9	3645	7 ADU83136	Adu83136 Human hem
22	1230	99.9	4495	6 ABU69135	Abu69135 Human NOV
23	1230	99.9	4495	8 ADH72106	Adh72106 Human PRO
24	1230	99.9	4495	8 ADO08273	Ado08273 Human NOV
25	1230	99.9	7112	8 ADH72104	Adh72104 Human PRO

1:02-01-03
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1	
ID	AAB47770 standard; peptide; 208 AA.
XX	
XX	
AC	AAB47770;
XX	
DT	04-MNR-2002 (first entry)
XX	
DE	Human thrombospondin protein, BTL.012, fragment 654-861.
XX	
KW	Human; thrombospondin; BTL.012; thrombospondin repeat domain; modulation;
KW	angiogenesis; cancer; metastasis; diabetic retinopathy;
KW	macular degeneration; cardiovascular disease; wound.
XX	
Homo sapiens.	
OS	
XX	
PN	WO200174952-A2.
XX	
PD	11-OCT-2001.
XX	
PF	30-MAR-2001; 2001WO-US010222.
XX	
PR	31-MNR-2000; 2000US-0266300F.
XX	
(FARB) BAYER CORP.	
PA	
XX	
PI	Chen J, Chen D, Zolotorev A, Davies CJ, Wetzel GD; Dubois-Stringfellow NA;
PI	
XX	
DR	WPI: 2002-066297/09.
XX	
CC	This sequence represents a fragment of the human thrombospondin protein, BTL.012. This peptide, comprising a thrombospondin repeat domain, may be used to modulate angiogenesis at a site. This BTL.012 fragment may be used for diagnosing, preventing or treating a medical condition, particularly cancer, metastasis, diabetic retinopathy, macular degeneration, cardiovascular disease or a wound.
CC	
PT	Sequence 208 AA;
SQ	
PS	Claim 2: Page 35: 54pp; English.
XX	
CC	This sequence represents a fragment of the human thrombospondin protein, BTL.012. This peptide, comprising a thrombospondin repeat domain, may be used to modulate angiogenesis at a site. This BTL.012 fragment may be used for diagnosing, preventing or treating a medical condition, particularly cancer, metastasis, diabetic retinopathy, macular degeneration, cardiovascular disease or a wound.
CC	
PT	Sequence 208 AA;
SQ	
PS	Query Match 100.0%; Score 1231; DB 5; Length 208;
XX	
CC	Best Local Similarity 100.0%; Pred. No. 9.9e-89;

Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QVHGGFSSWAVRACSYTCGKIQRSRLCNQPLANGKPCQGSDLEMNCNQKPCPVD 60
 DB 1 QVHGGFSSWAVRACSYTCGKIQRSRLCNQPLANGKPCQGSDLEMNCNQKPCPVD 60
 QY 61 GSWEWSLWEETRSQRGNOTRTTCTNNSVQCGGRPGCNAVEITMCNTRCPVHGAW 120
 DB 61 GSWEWSLWEETRSQRGNOTRTTCTNNSVQCGGRPGCNAVEITMCNTRCPVHGAW 120
 QY 121 SAQWPWGTCSESCKGKSTQTLRCLCNPPAFGGSYCDGAETOMQCNERNCPFHGRWAW 180
 DB 121 SAQWPWGTCSESCKGKSTQTLRCLCNPPAFGGSYCDGAETOMQCNERNCPFHGRWAW 180
 QY 181 ASWSACSVSCGGARORTRGCSDPVHQY 208
 DB 181 ASWSACSVSCGGARORTRGCSDPVHQY 208

RESULT 2

ABU69134 standard; protein; 707 AA.

XX

ABU69134;

DT 02-JUN-2003 (first entry)

XX Human NOVX polypeptide #9.

Human; NOVX; metabolic disorder; diabetes; infectious disease; obesity;
 anorexia; cancer; cardiovascular disorder; asthma; neurogenesis;
 neurodegenerative disorder; epilepsy; immune disorder; osteoarthritis;
 haematopoietic disorder; inflammatory skin disorder; dyslipidemia;
 viral infection; fungal infection; helminthic infection; atherosclerosis;
 protozoal infection; hypertension.
 Homo sapiens.

OS WO200290504-A2.

PN XX

PD 14-NOV-2-2002.

XX

PR 02-MAY-2002; 2002WO-US014342.

XX

PR 03-MAY-2001; 2001US-0288395P.

PR 04-MAY-2001; 2001US-0288900P.

PR 07-MAY-2001; 2001US-0289087P.

PR 09-MAY-2001; 2001US-0290753P.

PR 15-MAY-2001; 2001US-0291189P.

PR 16-MAY-2001; 2001US-0291243P.

PR 21-MAY-2001; 2001US-0292001P.

PR 22-MAY-2001; 2001US-0292374P.

PR 23-MAY-2001; 2001US-0293587P.

PR 29-MAY-2001; 2001US-029410P.

PR 30-MAY-2001; 2001US-0294434P.

PR 18-JUN-2001; 2001US-0294888P.

PR 31-JUL-2001; 2001US-0298888P.

PR 17-AUG-2001; 2001US-030801P.

PR 21-AUG-2001; 2001US-031851P.

PR 17-SEP-2001; 2001US-031937P.

PR 17-SEP-2001; 2001US-0322801P.

PR 25-SEP-2001; 2001US-0324157P.

PR 27-SEP-2001; 2001US-032514P.

PR 21-NOV-2001; 2001US-032682P.

PR 03-DEC-2001; 2001US-0332129P.

PR 14-DEC-2001; 2001US-034305P.

PR 01-MAY-2002; 2002US-00138588.

PA (CUBA-) CURAGEN CORP.

XX

PR Alsobrook JP, Anderson DW, Boldog FL, Burgess CE, Casman SJ;

PR Chapoval A, Edinger S, Gerlach V, Gorman L, Gunther E, Guo X;

PR Kekuta R, Lesley DM, Li L, Liu X, Malanykar UM, Miller CE,

PR Millet I, Padigaru M, Paturajan M, Pena CEA, Rieger DK,

PR Shirkets RA, Spytek KA, Taupier RJ, Vernet CAM, Voos EZ;

PR Zernhusen BD;

XX DR N-PSDB; ACA0119.

XX DR N-PSDB;

XX DR

DT	04-MAR-2002	(first entry)
XX	Human thrombospondin protein,	BTL_012.
DE		
XX	Human; thrombospondin;	BTL_012; thrombospondin repeat domain; modulation; angiogenesis; cancer; metastasis; diabetic retinopathy; macular degeneration; cardiovascular disease; wound.
KW		
XX	Homo sapiens.	
OS		
OS		
XX		
Key		Location/Qualifiers
FH		
FT	657..711	
FT	/label= thrombospondin domain type I repeat - a	
FT	714..768	
FT	/label= thrombospondin domain type I repeat - b	
Domain	771..825	
FT	/label= thrombospondin domain type I repeat - c	
FT	828..882	
FT	/label= thrombospondin domain type I repeat - d	
FT	885..939	
FT	/label= thrombospondin domain type I repeat - e	
Domain	942..996	
FT	/label= thrombospondin domain type I repeat - f	
FT	1325..1375	
Misc-difference		
FT	/label= Encoded by GAA	
FT		
XX		
PN	WO200174852-A2.	
XX		
XX	11-OCT-2001.	
PD	<u>30-MAR-2001</u> ; 2001WO-US010222.	
XX		
PF	31-MAR-2000; 2000US-0266300P.	
XX		
PR	(FARB) BAYER CORP.	
XX		
PA	Chen J, Chen D, Zolotorev A, Davies CJ, Wetzel GD;	
PI	Dubois-Stringfellow NA;	
PI		
XX		
DR	WPI: 2002-062297/09.	
XX		
DR	N/PSPDB; AAI72024.	
XX		
PT	Novel protein designated BTL_012 has a thrombospondin repeat and inhibits angiogenesis, and is useful to treat cancer, diabetic retinopathy, macular degeneration, cardiovascular disease and wounds.	
PT		
PT	Claim 21; Page 49-53; 54PP; English.	
XX		
PS		
XX	This sequence represents a human thrombospondin protein, BTL_012. A fragment of this protein, comprising a thrombospondin repeat domain, may be used to modulate angiogenesis at a site. The BTL_012 fragment may be used for diagnosing, preventing or treating a medical condition, particularly cancer, metastasis, diabetic retinopathy, macular degeneration, cardiovascular disease or a wound.	
SQ	Sequence 1336 AA;	
Query	Query Match	
Best Local Similarity	100.0%	Score 1231; DB 5; Length 1336;
Matches	1	Pred. No. 6..3e-88; Mismatches 0; Indels 0; Gaps 0
Conservative	0;	
Db	654	QVGGFSGSONSAMVACSYTICGKGTQTRKCNPNSYQHGRPCCEGNAVEIMCNTRCPVHGAW
Qy	654	QVGGFSGSONSAMVACSYTICGKGTQTRKCNPNSYQHGRPCCEGNAVEIMCNTRCPVHGAW
Db	654	QVGGFSGSONSAMVACSYTICGKGTQTRKCNPNSYQHGRPCCEGNAVEIMCNTRCPVHGAW
Qy	654	QVGGFSGSONSAMVACSYTICGKGTQTRKCNPNSYQHGRPCCEGNAVEIMCNTRCPVHGAW
Db	714	GSPSEWSLWEECTRSCEGNGNQTRTRTCNNPSPVQHGRPCCEGNAVEIMCNTRCPVHGAW
Qy	714	GSPSEWSLWEECTRSCEGNGNQTRTRTCNNPSPVQHGRPCCEGNAVEIMCNTRCPVHGAW
Db	714	GSPSEWSLWEECTRSCEGNGNQTRTRTCNNPSPVQHGRPCCEGNAVEIMCNTRCPVHGAW
Qy	714	SANQPWGTCSESLSCKGTQTRAKCNPPAFAGGSYCDGAETQMQVNCERNPPIHGKWWAT
Db	714	SANQPWGTCSESLSCKGTQTRAKCNPPAFAGGSYCDGAETQMQVNCERNPPIHGKWWAT
Qy	774	SANQPWGTCSESLSCKGTQTRAKCNPPAFAGGSYCDGAETQMQVNCERNPPIHGKWWAT
Db	774	SANQPWGTCSESLSCKGTQTRAKCNPPAFAGGSYCDGAETQMQVNCERNPPIHGKWWAT

Qy	RESULT 6 ADG39841 ID ADG39841 standard; protein; 1708 AA. XX	KW Human; NOVX; cardiomyopathy; atherosclerosis
AC	AC ADG39841; XX	KW congenital heart defect; pulmonary stenosis
CC	CC metabolic disturbance; obesity; transplant	KW adrenal hyperplasia; prostate
DT	DT 26-FEB-2004 (first entry) XX	KW metabolic disorder; neoplasm; adenocarcinoma
DB	DB Graft versus host disease; AIDS; bronchitis	KW multiple sclerosis; infectious disease
		KW neurodegenerative disorder; Alzheimer's disease
		KW immune disorder; haematopoietic disorder;
		KW wasting disorder.
		XX Homo sapiens.
		XX US2003203843-A1.
		XX PN
		XX PD 30-OCT-2003.
		XX PF 11-APR-2002; 2002US-00120801.
		XX PR 20-APR-2001; 2001US-0285609P.
		PR 23-APR-2001; 2001US-0285749P.
		PR 24-APR-2001; 2001US-0286168P.
		PR 25-APR-2001; 2001US-0286292P.
		PR 03-MAY-2001; 2001US-0288334P.
		PR 16-MAY-2001; 2001US-0291141P.
		PR 14-SEP-2001; 2001US-0322284P.
		XX PA (PENA,) PENA C E A.
		PA (GUOX,) GUO X.
		PA (SHIM,) SHIMKETS R. A.
		PA (PADIGARU,) PADIGARU M.
		PA (KEKU,) KERKU R.
		PA (SPYT,) SPYTEK K A.
		PA (MEHR,) MEHRABAN F.
		PA (TOPP,) TOPPER J N.
		PA (MALY,) MALYANKAR U M.
		PA (WASS,) WASSERMAN S M.
		PA (EDIN,) EDINGER S R.
		PA (SMIT,) SMITHSON G.
		PA (GUNT,) GUTHIER E.
		PA (KOMU,) KOMUVES L.
		XX PI Peng CEA, Guo X, Shimkets RA, Padigaru, PI Nehrban F, Topper JN, Malyankar UM, PI Smithson G, Gunther E, Komuves L;
		XX DR WPI: 2003-900671/82.
		XX PT New NOVX polypeptides and nucleic acids.
		PT The invention relates to a new isolated polypeptide selected from a library fully defined by the sequence set forth in claim 1.
		CC CC The invention relates to a new isolated polypeptide selected from a library fully defined by the sequence set forth in claim 1.
		CC CC NOS between ADG39770 and ADG39802.
		PT Obesity, prostate cancer, AIDS, bronchitis, multiple sclerosis.
		PT Disclosure; SEQ ID NO 73; 215pp; English
		PS XX

CC amino acid or a variant of NOVX, where one or more amino acid residue in
 CC the variant differs in no more than 15% of the amino acid residues of
 CC NOVX. Also included are an isolated nucleic acid (NA) molecule
 CC (comprising a nucleic acid sequence encoding a NOVX polypeptide above
 CC (odd SEQ ID NOS between ADG3769 and ADG39801), a nucleic acid fragment
 CC encoding at least a portion of a NOVX polypeptide and a complement of
 CC NOVX NA, a vector comprising NOVX NA, a cell comprising the vector, an
 CC antibody that immunospecifically binds to NOVX, a method for determining
 CC the presence or amount of NOVX or NOVX NA in a sample, a method of
 CC identifying an agent that binds to NOVX, a method for identifying an
 CC agent that modulates the expression or activity of NOVX, a method for
 CC modulating the activity of NOVX, a method of treating or preventing a
 CC NOVX-associated disorder, a method for screening for a modulator of
 CC activity or of latency or predisposition to a NOVX-associated disorder, a
 CC method for determining the presence of or predisposition to a disease
 CC associated with altered levels of NOVX or NOVX NA in a first mammalian
 CC subject and a method of treating a pathological state in a mammal by
 CC administering NOVX or an antibody that binds to NOVX. The NOVX
 CC polypeptide, nucleic acid or antibody is useful in the manufacture of a
 CC medicament for treating a syndrome associated with a human disease or a
 CC NOVX-associated disorder. The NOVX polypeptides and nucleic acids
 CC encoding them are useful for diagnosing or treating pathologies, diseases
 CC or conditions associated with NOVX sequences, including cardiomyopathy,
 CC atherosclerosis, hypertension, congenital heart defects, pulmonary
 CC stenosis, scleroderma, obesity, metabolic disturbances associated with
 CC hyperplasia, transplantation, adenoleukodystrophy, congenital adrenal
 CC adenocarcinoma, fertility, haemophilia, graft versus host disease, AIDS,
 CC bronchial asthma, Crohn's disease, multiple sclerosis, infectious
 CC disease, anorexia, neurodegenerative disorders (e.g. Alzheimer's disease,
 CC or Parkinson's disease), immune disorders, haemopoietic disorders,
 CC dyslipidaemias, and wasting disorders associated with chronic diseases.
 CC The polypeptides can be used as immunogens to produce antibodies and as
 CC vaccines. The sequences may further be used in chromosome mapping,
 CC identifying individual from minute biological samples (tissue typing),
 CC and in forensic identification of a biological sample. The present
 CC sequence is a protein showing sequence similarity to a NOVX protein.
 XX Sequence 1708 AA;
 SQ 100.0%; Score 1231; DB 7; Length 1708;
 Best Local Similarity 100.0%; Pred. No. 8e-38;
 Matches 208; Conservative 0; Mismatches 0; Gaps 0;

Db 660 1 QVHGGESQWAWRACSVTCCGGIQRSRLNQPLANGGICPQCGSDLENRNCQNPKCPVD 60
 Db 660 600 QVHGGESQWAWRACSVTCCGGIQRSRLNQPLANGGICPQCGSDLENRNCQNPKCPVD 659

Qy 61 GSWEENLWEEETRSRGNGTRTCNNPSVQHGRPCGNAEVIIIMCNTRPCPVHGAW 120

Db 660 GSWEENLWEEETRSRGNGTRTCNNPSVQHGRPCGNAEVIIIMCNTRPCPVHGAW 719

Qy 121 SAQWPCTCSBEGKCTQRARLCNNPPAFEGGSTCDGAFTOMQVCNERNCPITHGKWTW 180

Db 720 720 SAQWPCTCSBEGKCTQRARLCNNPPAFEGGSTCDGAFTOMQVCNERNCPITHGKWTW 779

Qy 181 ASWSACSVSCEGGAAORTRGCDSPVHQY 208

Db 780 780 ASWSACSVSCEGGAAORTRGCDSPVHQY 807

Query Match Score 1231; DB 7; Length 1708;
 Best Local Similarity 100.0%; Pred. No. 8e-38;
 Matches 208; Conservative 0; Mismatches 0; Gaps 0;

XX Pena CBA, Guo X, Shimkets RA, Padigaru M, Kekuda R, Sptyek KA;
 PI Nebraban F, Topper JN, Malyankar UM, Wasserman SM, Edlinger SR;
 PI Smithson G, Gunther E, Komives L;

XX WPI: 2003-900671/82.

XX Disclosure: SEQ ID NO 72; 215pp; English.

XX The invention relates to a new isolated polypeptide comprising an amino
 CC acid sequence selected from 17 fully defined human NOVX sequences (even
 CC SEQ ID NOS between ADG39770 and ADG39802), a mature form of the NOVX
 CC amino acid or a variant of NOVX, where one or more amino acid residue in
 CC the variant differs in no more than 15% of the amino acid residues of
 CC NOVX. Also included are an isolated nucleic acid (NA) molecule
 CC (comprising a nucleic acid sequence encoding a NOVX polypeptide above
 CC (odd SEQ ID NOS between ADG39769 and ADG39801), a nucleic acid fragment
 CC encoding at least a portion of a NOVX polypeptide and a complement of
 CC NOVX NA), a vector comprising NOVX NA, a cell comprising the vector, an
 CC antibody that immunospecifically binds to NOVX, a method for determining
 CC the presence or amount of NOVX or NOVX NA in a sample, a method of
 CC identifying an agent that binds to NOVX, a method for identifying an
 CC agent that modulates the expression or activity of NOVX, a method for
 CC modulating the activity of NOVX, a method of treating or preventing a
 CC NOVX-associated disorder, a method for screening for a modulator of
 CC activity or of latency or predisposition to a NOVX-associated disorder, a
 CC method for determining the presence of or predisposition to a disease
 CC associated with altered levels of NOVX or NOVX NA in a first mammalian
 CC subject and a method of treating a pathological state in a mammal by

CC RESULT 7 DT 26-FBB-2004 (First entry)
 CC ID ADG39840 standard; protein: 1708 AA.
 CC Protein similar to human NOY9 #1.

XX Human; NOVX; cardiomyopathy; atherosclerosis; hypertension; scleroderma; obesity;
 KW congenital heart defect; pulmonary stenosis; scleroderma; obesity;

QY 61 GSWSWSLNEFFECTSGRGNQTRTRTCNNPSVQHGGRCPEGNAYEILMONIRPCPVHGAW 120
 Db 9711 GSWSWSLWEBCTRSCGRNQTRTRTCNNPSVQHGGRCPEGNAYEILMONIRPCPVHGAW 1030

QY 121 SAWQWGTSESCCGKTQTRARLNPPAFGSYCDAEATONQCVNCERNCP1HGRWATW 180
 Db 1031 SAWQWGTSESCCGKTQTRARLNPPAFGSYCDAEATONQCVNCERNCP1HGRWATW 1090

QY 181 ASWACSVCGGARQRTGCSDFVPQY 208
 Db 10911 ASWSACSVCGGARQRTGCSDFVPQY 1118

RESULT 9
 ADH72108 standard; protein; 1902 AA.
 XX ADH72108
 AC AC
 XX DT 25-MAR-2004 (first entry)
 XX DE Human protein of the invention NOV43d SEQ ID NO:1004.
 XX KW human; cytostatic; immunomodulator; neuroprotective; nootropic;
 KW anorectic; antidiabetic; antimicrobial; antiinflammatory; gene therapy;
 KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
 KW obesity; diabetes; infectious disease; metabolic syndrome X;
 KW dyslipidaemia.
 XX OS Homo sapiens.
 XX PN WO2003102155-A2.
 XX PD 11-DEC-2-2003.
 XX PF 03-JUN-2003; 2003WO-US017430.
 XX PR 03-JUN-2002; 2002US-0385120P.
 PR 04-JUN-2002; 2002US-0385744P.
 PR 05-JUN-2002; 2002US-0386041P.
 PR 06-JUN-2002; 2002US-0386047P.
 PR 06-JUN-2002; 2002US-0386376P.
 PR 06-JUN-2002; 2002US-0386453P.
 PR 06-JUN-2002; 2002US-0386844P.
 PR 07-JUN-2002; 2002US-0386844P.
 PR 07-JUN-2002; 2002US-0386844P.
 PR 07-JUN-2002; 2002US-0386844P.
 PR 07-JUN-2002; 2002US-0386931P.
 PR 07-JUN-2002; 2002US-0386942P.
 PR 07-JUN-2002; 2002US-0386971P.
 PR 08-JUN-2002; 2002US-0387262P.
 PR 10-JUN-2002; 2002US-0296940P.
 PR 10-JUN-2002; 2002US-0387400P.
 PR 11-JUN-2002; 2002US-0387535P.
 PR 11-JUN-2002; 2002US-037810P.
 PR 11-JUN-2002; 2002US-0387625P.
 PR 11-JUN-2002; 2002US-0387634P.
 PR 11-JUN-2002; 2002US-0387668P.
 PR 11-JUN-2002; 2002US-0387696P.
 PR 11-JUN-2002; 2002US-0387702P.
 PR 11-JUN-2002; 2002US-0387836P.
 PR 12-JUN-2002; 2002US-0387859P.
 PR 12-JUN-2002; 2002US-0387934P.
 PR 12-JUN-2002; 2002US-0387960P.
 PR 12-JUN-2002; 2002US-0388022P.
 PR 12-JUN-2002; 2002US-0388066P.
 PR 13-JUN-2002; 2002US-0389123P.
 PR 14-JUN-2002; 2002US-0389118P.
 PR 14-JUN-2002; 2002US-0389120P.
 PR 14-JUN-2002; 2002US-0389144P.
 PR 14-JUN-2002; 2002US-0389146P.
 PR 17-JUN-2002; 2002US-038929P.

PR 17-JUN-2002; 2002US-038942P.
 PR 18-JUN-2002; 2002US-038984P.
 PR 19-JUN-2002; 2002US-039006P.
 PR 20-JUN-2002; 2002US-0390209P.
 PR 21-JUN-2002; 2002US-0390763P.
 PR 17-JUL-2002; 2002US-0396706P.
 PR 09-AUG-2002; 2002US-0401628P.
 PR 09-AUG-2002; 2002US-040256P.
 PR 09-AUG-2002; 2002US-040289P.
 PR 12-AUG-2002; 2002US-0402816P.
 PR 12-AUG-2002; 2002US-0402821P.
 PR 13-AUG-2002; 2002US-040348P.
 PR 13-AUG-2002; 2002US-040351P.
 PR 13-AUG-2002; 2002US-0403532P.
 PR 13-AUG-2002; 2002US-0403563P.
 PR 13-AUG-2002; 2002US-040617P.
 PR 26-AUG-2002; 2002US-0406182P.
 PR 26-AUG-2002; 2002US-0406355P.
 PR 27-AUG-2002; 2002US-0406240P.
 PR 20-SEP-2002; 2002US-0410084P.
 PR 20-SEP-2002; 2002US-0412528P.
 PR 30-SEP-2002; 2002US-0412731P.
 PR 30-SEP-2002; 2002US-0414801P.
 PR 30-SEP-2002; 2002US-0414839P.
 PR 30-SEP-2002; 2002US-0414840P.
 PR 09-OCT-2002; 2002US-0414954P.
 PR 09-OCT-2002; 2002US-0417186P.
 PR 23-OCT-2002; 2002US-0417440P.
 PR 28-OCT-2002; 2002US-0421166P.
 PR 31-OCT-2002; 2002US-0422600P.
 PR 01-NOV-2002; 2002US-042310P.
 PR 05-NOV-2002; 2002US-0423198P.
 PR 05-NOV-2002; 2002US-0423798P.
 PR 12-NOV-2002; 2002US-0425433P.
 XX (CURA-) CURAGEN CORP.
 XX PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
 Catterton E, Chapoval A, Crabtree Bokor JR, Edinger SR, Ellerman K;
 Ettemberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
 Gusev VI, Herriman JL, Jui W, Kekuda R, Li L, Liu X, Macdougal JR;
 MacLachlan T, Malanykar UM, Mezick AJ, Millet I, Mishra VS;
 Padigaru M, Paturajan M, Pena CBA, Peyman JA, Rana D, Rastelli L;
 Rieger DK, Rothenberg ME, Sciore P, Shemket RA, Smithets G, Spyke KA, Stone DJ, Vernet CM, Voss EZ, Zhong M;
 PR WPI; 2004-081935/08.
 XX N-PSDB; ADH72107.

XX The invention relates to a novel isolated polypeptide (NOVX). A polypeptide of the invention has cytosolic, immunomodulator, antiinflammatory, nootropic, anorectic, antimicrobial, and neuroprotective activity, and may have a use in gene therapy, and as a vaccine. The polypeptides are encoded by NOVX polynucleotides comprising any of the 303 fully defined nucleotide sequences given in the specification. The polypeptide is useful in the manufacture of a medicament for treating a syndrome associated with a human disease. The polypeptide, polynucleotide and antibody are useful in diagnosing, treating or preventing NOVX-associated disorders e.g., cancer, cachexia, Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious

XX PI New NOVX polypeptides and nucleic acid molecules useful for preventing or treating NOVX-associated disorders, e.g., cancer, diabetes, infection or obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

XX Example 43; SEQ ID NO 1004; 1880pp; English.

XX The invention relates to a novel isolated polypeptide (NOVX). A polypeptide of the invention has cytosolic, immunomodulator, antiinflammatory, nootropic, anorectic, antimicrobial, and neuroprotective activity, and may have a use in gene therapy, and as a vaccine. The polypeptides are encoded by NOVX polynucleotides comprising any of the 303 fully defined nucleotide sequences given in the specification. The polypeptide is useful in the manufacture of a medicament for treating a syndrome associated with a human disease. The polypeptide, polynucleotide and antibody are useful in diagnosing, treating or preventing NOVX-associated disorders e.g., cancer, cachexia, Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious

diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are further used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The present sequence represents a NO_{XY} polypeptide of the invention.

Sequence 1902 AA:

```

Query Match      100.0%; Score 1231; DB 8; Length 1902;
Best Local Similarity 100.0%; Pred. No. 9e-88;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY          1 QVHGGSSQWSAWRACSVTCKG1QKRSRLNQPLDANGSKPCCOISDLIIMRNCONKCPV р
Db          911 QVHGGSSQWSAWRACSVTCKG1QKRSRLNQPLDANGSKPCCOISDLIIMRNCONKCPV р
Db          971 GSWSNSLWBECTRSGRGNQTRTCTNNPSVQHGRPEGAIVEILMCNIRCPV р
QY          61 GSWSNSLWBECTRSGRGNQTRTCTNNPSVQHGRPEGAIVEILMCNIRCPV р
Db          971 GSWSNSLWBECTRSGRGNQTRTCTNNPSVQHGRPEGAIVEILMCNIRCPV р
QY          121 SAWPQPGTCSSCGKGTQTRARLCNNPAPFGGSYCDGAETQMVCNERNCPTHGKWTW 180
Db          1031 SAWPQPGTCSSCGKGTQTRARLCNNPAPFGGSYCDGAETQMVCNERNCPTHGKWTW 1090
QY          181 ASWSACSVSCGGAAQRTRGCSDPV р
Db          1091 ASWSACSVSCGGAAQRTRGCSDPV р

```

RESULT 10
ID ABP6091 standard; protein: 5635 AA.
AC ABP6091;
DT 10-SEP-2002 (first entry)
DB Novel human protein. SEQ ID 78.
XX Human; cyrostatic; vulnerability; antiarteriosclerotic; antiparkinsonian;
KW nootropic; neuroprotective; immunosuppressive; haemostatic;
KW antiinflammatory; cardioton; antiulcer; viricide; antithyroid;
KW cerebroprotective; anorectic; metabolic; vaccine; cancer; infection;
KW wound healing disorders; atherosclerosis; Parkinson's disease;
KW Alzheimer's disease; autoimmunity; haematopoietic disorder;
KW inflammation; neoplastic disease; nervous system disorder;
KW cardiovascular disorders; pancreatitis; respiratory disorder;
KW hyperproliferation; systemic autoimmune disease; hyper-immunity;
KW developmental abnormality; gastrointestinal ulceration; neuropathy;
KW haematological disease; metabolic disease; sperm dysfunction;
KW thyroid disorder; hypothyroidism; brain damage; colitis;
KW cone Photo-transduction deficiency; neurological disease; stroke;
KW angiogenesis; ovulation disorder; spinal cord; thyroid gland; heart;
KW trachea; thymus; lymph node; muscular system; obesity; anorexia;
KW growth abnormalities and alleviation of precocious puberty. The
XX Homo sapiens.

XX WO2002050105-A1.
XX 27-JUN-2002.
DD 17-DEC-2001; 2801WO-US049232.
PF XX 19-DEC-2000; 2000US-0256710P.
PR 20-DEC-2000; 2000US-0257048P.
PR 09-JAN-2001; 2001US-0260482P.
PR 30-JAN-2001; 2001US-0264922P.
PR 06-FEB-2001; 2001US-0266797P.
PR 19-MAR-2001; 2001US-027598P.
PR 04-APR-2001; 2001US-0281535P.
PR 08-MAY-2001; 2001US-028862P.
XX (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.
XX PI Agarwal P, Birkeland M, Cogswell JP, Kabnick KP, Lai Y,
PI Martensen SA, Rizvi SK, Sturm JC, Xie Q,
XX DR WPI; 2002-5087454.
DR N-PDB; ABQ86156.
XX PT Secreted proteins and polynucleotides useful as vaccines for preventing
PT or treating various diseases e.g. cancer, wounds, atherosclerosis,
PT Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder.
XX PS Claim 1(a); Page 285-297; 335pp; English.
XX CC The invention relates to an isolated polypeptide with signal sequences
CC which allow it to be secreted extracellularly or membrane associated. The
CC activity of polypeptides of the invention may be described as,
CC cytotoxic, vulnerary, antiarteriosclerotic, antiparkinsonian, nootropic,
CC neuroprotective, immunosuppressive, haemostatic, antiinflammatory,
CC cardioton, antiulcer, viricide, antithyroid, Cerebroprotective, anorectic,
CC and metabolic. Polypeptides and polynucleotides of the invention are
CC useful in the treatment, or as a vaccine in the prevention of, cancer,
CC wound healing disorders, infection, atherosclerosis, Parkinson's disease
CC and Alzheimer's disease, autoimmunity, haematopoietic disorder,
CC inflammation, neoplastic diseases, nervous system related disorders and
CC cardiovascular disorders, diseases in the spinal cord, thyroid gland, heart,
CC hyperproliferation, systemic autoimmune disease, hyper immunity,
CC developmental abnormality, gastrointestinal ulceration, neuropathy,
CC haematological diseases, metabolic disease, sperm dysfunction, thyro-
CC idisorders e.g. hypothyroidism, brain damage, colitis, cone phototo-
CC transduction deficiency, neurological diseases, stroke, angiogenesis,
CC ovulation disorders, diseases in the spinal cord, thyroid gland, heart,
CC trachea, thymus, lymph node and muscular system, obesity, anorexia,
CC growth abnormalities and alleviation of precocious puberty. The
CC sequences given in records ABP6095-ABP6109 represent novel human
CC proteins of the invention.

XX Sequence 5635 AA:
Query Match 100.0%; Score 1231; DB 5; Length 5635;
Best Local Similarity 100.0%; Pred. No. 2.6e-87;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVHGGSSQWSAWRACSVTCKG1QKRSRLNQPLDANGSKPCCOISDLIIMRNCONKCPV р
Db 4527 QVHGGSSQWSAWRACSVTCKG1QKRSRLNQPLDANGSKPCCOISDLIIMRNCONKCPV р
Db 61 GSNEWSLWBECTRSGRGNQTRTCTNNPSVQHGRPEGAIVEILMCNIRCPV р
Db 4587 GSNEWSLWBECTRSGRGNQTRTCTNNPSVQHGRPEGAIVEILMCNIRCPV р
Db 121 SANOPWGTCSESCGGAAQRTGCSDPV р
Db 4647 SANOPWGTCSESCGGAAQRTGCSDPV р

RESULT 11.
ADJ70089
ID ADJ70089 standard; protein: 5636 AA.
XX ADJ70089;
AC
XX DT 06-MAY-2004 (first entry)
DE Human heat mitochondrial protein as a therapeutic target SeqID1895.
XX KW mitochondrial; human; screening assay; diabetes mellitus;
KW Huntington's disease; osteoarthritis;

Leber's hereditary optic neuropathy; LHON;
 KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
 KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
 KW neuroprotective; nocropic; antidiabetic; anticancer;
 KW osteopathic; opthalmological; Cystostatic;
 XX OS Homo sapiens.
 XX PN WO2003087768-A2.
 XX PD 23-OCT-2003.
 XX PF 04-APR-2003; 2003WO-US010870.
 XX PR 12-APR-2002; 2002US-0372843P.
 PR 17-JUN-2002; 2002US-038997P.
 PR 20-SEP-2002; 2002US-0412418P.
 XX PA (MITO-) MITOKOR.
 PA (BUCK-) BUCK INST AGE RES.
 XX Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM,
 PI Warnock DE;
 DR WPI: 2003-845369/78.
 XX PT Identifying a mitochondrial target for drug screening assays and for
 PT treating diseases associated with altered mitochondrial function, and correlating
 PT comprises detecting a modified polypeptide in a sample and correlating
 PT with the disease.
 XX Claim 1: SEQ ID NO 1895; 180pp; English.
 XX This invention relates to novel mitochondrial targets that can be used
 CC for therapeutic intervention in treating a disease associated with
 CC altered mitochondrial function. Specifically, it refers to a method for
 CC identifying proteins of the human heart mitochondrial proteome that are
 CC useful for drug screening assays, as well as therapeutic targets. The
 CC present invention describes method for identifying such proteins that
 CC can be used in the treatment of various diseases associated with altered
 CC mitochondrial function including diabetes mellitus, Huntington's disease,
 CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
 CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
 CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
 CC compositions have neuroprotective, nocropic, antidiabetic,
 CC anticonvulsant, antiarthritic, osteopathic, opthalmological and
 CC mitochondrial protein of the invention.
 XX SQ Sequence 5636 AA;
 Qy Query Match Score 1231; DB 7; Length 5636;
 Best Local Similarity 100.0%; Pred. No. 2.6e-87.
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 QVHGGESQWSAWRACSVTCGGIQKRSRLCNPQLDANGGPGCGSDLLENRCNQNRCPVTD 60
 4528 QVHGGESQWSAWRACSVTCGGIQKRSRLCNPQLDANGGPGCGSDLLENRCNQNRCPVTD 4587
 Qy 61 GSWESESLWEBTTRSGRGNQTRTCNNPSVQHGRPCCEGNAVEIIMCNIRPCPVIGAW 120
 Db 4588 GSWESESLWEBTTRSGRGNQTRTCNNPSVQHGRPCCEGNAVEIIMCNIRPCPVIGAW 4647
 Qy 121 SAQWPNGTCSESQKGTQHARLCNNPPFGSYCDGAETQMCNERNCPTHGKWA 180
 Db 4648 SAQWPNGTCSESQKGTQHARLCNNPPFGSYCDGAETQMCNERNCPTHGKWA 4707
 Qy 181 ASWSACSVSCGGARQRTRGCDPVPQY 208
 Db 4708 ASWSACSVSCGGARQRTRGCDPVPQY 4735

ADU83137
 ID ADU83137 standard; protein; 5636 AA.
 XX AC ADU83137;
 XX DT 06-MAY-2004 (First entry)
 DE Human hemicentin protein - SEQ ID 128.
 XX KW NOVK; cytostatic; antiarteriosclerotic; antidiabetic; antiasthmatic;
 KW antiallergic; antiinflammatory; respiratory; antiarthritic;
 KW dermatological; antibacterial; cerebroprotective; vasotropic; cardiotonic;
 KW haemostatic; hypotensive; hepatotropic; neuroprotective; anorectic;
 KW nootropic; antilulcer; muscular; immunosuppressive; gynaecological;
 KW antiparkinsonian; endocrine; opthalmological; osteopathic;
 KW anticonvulsant; tranquiliser; analgesic; nephrotropic;
 KW antifertility; antilaemic; cardionopathy; atherosclerosis; diabetes;
 KW cell signal processing; metabolic pathway; asthma; allergy; emphysema;
 KW autoimmune; graft-versus-host; arthritis; stroke; haemophilia;
 KW obesity; Alzheimer's; pain; chromosome mapping; tissue typing; human;
 KW hemicentin.
 XX OS Homo sapiens.
 XX PN US2003170630-A1.
 XX PD 11-SEP-2003.
 XX FF 21-DEC-2001; 2001US-00032189.
 XX PR 21-DEC-2000; 2000US-0257495P.
 PR 22-DEC-2000; 2000US-0258171P.
 PR 20-FEB-2001; 2001US-0269940P.
 PR 08-MAR-2001; 2001US-0274192P.
 PR 22-MAR-2001; 2001US-0277826P.
 PR 29-MAR-2001; 2001US-0279840P.
 PR 11-APR-2001; 2001US-028181P.
 PR 13-APR-2001; 2001US-0283656P.
 PR 31-JUL-2001; 2001US-0309241P.
 PR 10-AUG-2001; 2001US-031154P.
 PR 17-AUG-2001; 2001US-031331P.
 XX PA (ALSOBROOK J. P.
 PA (TCHENIEV V. T.
 PA (LIU X.
 PA (SPYTEK K. A.
 PA (ZERHUSEN B. D.
 PA (PATTURAJAN M.
 PA (LEPLEY D. M.
 PA (BURGESE C. E.
 PA (SHIMKETS R. A.
 PA (GROSSE W. M.
 PA (SZEKERES E. S.
 PA (VERN) VERNET C A. M.
 PA (LILL) LI L.
 PA (CASM) CASMAN S. J.
 PA (BOLD) BOLDIG F. L.
 PA (GORM) GORMAN L.
 PA (GANG) GANGOLLI E. A.
 PA (PERIN) PERINANDS E. R.
 PA (RIEG) RIEGER D. K.
 PA (EDIN) EDINGER S. R.
 PA (GUNT) GUNTHER E.
 PA (MILL) MILLET L.
 PA (SCIO) SCIORE P.
 PA (BELL) BELLERMAN K.
 PA (MACD) MACDOUGALL J. R.
 PA (SMIT) SMITHSON G.
 XX
 Alsobrook JP, Tchernev VT, Liu X, Spytek KA, Zerhusen BD, Grossé WM;
 PI Paturajan M, Lepley DM, Burgess CE, Shimkets RA, Grossé WM;
 PI Szekeres ES, Vernet CM, Li L, Casman SJ, Boldig FL, Gorman L, Edinger SR, Gunther E;
 RESULT 12

XX	06-MAY-2004	(first entry)	Db	4648	SAWQPNGTCSSCGKGQTQARLCLNNPPAEGGSDPYPQY	208
DE	Angiogenesis differentially expressed protein GS-P29.		Qy	181	ASWSAcSVSCGGAPQRTGCGSDPYPQY	208
XX	vasotropin; antirheumatic; antiarthritic; hypotensive; antianginal;		Db	4708	ASWSAcSVSCGGARQRTGCGSDPYPQY	4735
KW	antiinflammatory; cardiant; angiogenesis inhibitor; gene therapy;					
KW	angiogenesis; endothelial cell; diagnosis; tumor vascularization;					
KW	retinopathy; rheumatoid arthritis; Crohn's disease; atherosclerosis;					
KW	ovary hyperstimulation; psoriasis; endometriosis; restenosis;					
KW	angioplasty; cataractation; peripheral vascular disease; hypertension;					
KW	vascular inflammation; Raynaud's disease; aneurism; thrombolebitis;					
KW	ischemia; angina; myocardial infarction; chronic heart disease;					
XX	cardiac congestion; macular degeneration; osteoporosis.					
OS	Homo sapiens.					
PN	FR2836686-A1.					
XX	PT 05-SEP-2003.					
XX	PT 04-MAR-2002; 2002FR-000002717.					
PR	04-MAR-2002; 2002FR-000002717.					
XX	(GENE-) GENE SIGNAL.					
PA	(ALMA-) AL MAHMOOD S.					
XX	Colin S, Schneider C, Al Mahmood S;					
PT	WPI: 2004-013911/02.					
DR	N-PSDB; ADK60756.					
XX	Compositions containing nucleic acid or polypeptide differentially expressed in angiogenesis are useful to diagnose, prognose and treat angiogenic disorders including tumor vascularization and heart disease.					
PS	Claim 7; SEQ ID NO 81; 405pp; French.					
XX	The invention relates to a novel pharmaceutical composition active on angiogenesis comprising an endothelial cell nucleic acid whose expression is induced by an angiogenic factor and inhibited by an angiostatic agent or its complement or fragment, a polypeptide sequence encoded by the nucleic acid or its fragment, a molecule capable of inhibiting expression of the nucleic acid or a molecule which binds to the polypeptide sequence. The invention is used to diagnose, prognose or treat an angiogenic disorder in a mammal, particularly a human. The disorder is particularly tumor vascularization, a retinopathy, rheumatoid arthritis, Crohn's disease, atherosclerosis, ovary hyperstimulation, psoriasis, endometriosis associated with neovascularization, restenosis due to angioplasty, overproduction of tissue due to cicatrisation, a peripheral vascular disease, hypertension, vascular inflammation, Raynaud disease, aneurism, arterial restenosis, thrombolebitis, ischemia, angina, myocardial infarction, chronic heart disease, cardiac congestion or macular degeneration due to age or osteoporosis. This sequence corresponds to a protein encoded by a differentially expressed DNA used in the composition of the invention.					
XX	Sequence 5636 AA;					
SQ	Query Match Similarity 100.0%; Score 1231; DB 8; Length 5636;					
Best Local Similarity 100.0%; Pred. No 2.6e-87;						
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
Qy	1 QVHGGFSQWAWRACSVTCCGKGQTQPLANGKPCQOQDLEMNRNCNQKPCPYD 60					
Db	4528 QVHGGFSQWAWRACSVTCCGKGQTQPLANGKPCQOQDLEMNRNCNQKPCPYD 4587					
Qy	61 GSWSSENSLWEEFCTRSGRGNQTRTRTCNNVSQHGRPCQEGNAVEIIMCNIRPPVHAW 120					
Db	4588 GSWSSENSLWEEFCTRSGRGNQTRTRTCNNVSQHGRPCQEGNAVEIIMCNIRPPVHAW 4647					
Qy	121 SAWQPNGTCSSCGKGQTQARLCLNNPPAEGGSDPYPQY					

vector. The angiogenesis inhibitor has the following activities:
 CC antiangiogenic, angiogenesis stimulator, angiogenesis inhibitor,
 CC cytostatic, dermatological, antiarthritic, antirheumatic,
 CC antiinflammatory, vasoconstrictive, hypotensive, ophthalmological,
 CC anti-psoriatic, and cardiotonic. The novel nucleic acid molecules of the
 CC invention may be used to treat disorders in gene therapy and antisense
 CC gene therapy. The nucleic acid sequences, proteins and antibodies as part
 CC of the therapeutic compositions are useful in treating a disorder of
 CC angiogenesis chosen from: tumour vascularisation, retinopathies,
 CC rheumatoid arthritis, Crohn's disease, atherosclerosis, ovarian
 CC hyperstimulation, psoriasis, endometriosis associated with
 CC neovascularisation, restenosis due to balloon angioplasty, tissue
 CC granulation due to scarification, peripheral vascular disorders,
 CC hypertension, vascular inflammation, Raynaud's disease, aneurism,
 CC arterial restenosis, thromboangiitis, lymphadenopathy, lymphedema,
 CC ischaemia, angina, myocardial infarct, chronic heart disease,
 CC congestive heart disease, muscular degeneration linked to age and
 CC osteoporosis. This sequence represents a human protein for the creation
 CC of an angiogenesis inhibitor of the invention.

xx

Sequence 5636 AA;

	Query Match	Score	Length
QY	1 QVHGGFSQWAWAATSVTCGKGTOQRSLRQCNPQLPANGKPCGSDLEMRNQNRCPV	1231	DB 8;
Db	4528 QVHGGPSQWAWAATSVTCGKGTOQRSLRQCNPQLPANGKPCGSDLEMRNQNRCPV	100.0%	Best Local Similarity
QY	61 GSWSSEWSLMEBCTRSGRENQTRTCNPNPSVHGGPCEGNAVEITIMCNIRPCPVHGAW	100.0%	Conservative
Db	4588 GSWSSEWSLMEBCTRSGRENQTRTCNPNPSVHGGPCEGNAVEITIMCNIRPCPVHGAW	0	Matches
QY	121 SAWQFWGTCSBSCCGKGTOQRSLRQCNPPLAFCGSYCDGAETONQVCNERNCPIGHKWTW	0	Mismatches
Db	4648 SAWQFWGTCSBSCCGKGTOQRSLRQCNPPLAFCGSYCDGAETONQVCNERNCPIGHKWTW	0	Indels
QY	181 ASWSACSVSFGGAGARQRTGCSDPVPOY	0	Gaps
Db	4708 ASWSACSVSCGGARQRTGCSDPVQY	0	O:

1 QVHGGFSQWAWAATSVTCGKGTOQRSLRQCNPQLPANGKPCGSDLEMRNQNRCPV 60 ~
 4528 QVHGGPSQWAWAATSVTCGKGTOQRSLRQCNPQLPANGKPCGSDLEMRNQNRCPV 4587
 61 GSWSSEWSLMEBCTRSGRENQTRTCNPNPSVHGGPCEGNAVEITIMCNIRPCPVHGAW 120
 4588 GSWSSEWSLMEBCTRSGRENQTRTCNPNPSVHGGPCEGNAVEITIMCNIRPCPVHGAW 4647
 121 SAWQFWGTCSBSCCGKGTOQRSLRQCNPPLAFCGSYCDGAETONQVCNERNCPIGHKWTW 180
 4648 SAWQFWGTCSBSCCGKGTOQRSLRQCNPPLAFCGSYCDGAETONQVCNERNCPIGHKWTW 4707
 181 ASWSACSVSFGGAGARQRTGCSDPVPOY 208
 4708 ASWSACSVSCGGARQRTGCSDPVQY 4735

Search completed: November 17, 2004, 15:52:22
 Job time : 175 secs



OM protein - protein search, using sw model

Run on: November 17, 2004, 15:49:06 ; Search time 39 Seconds
(without alignments)
353.696 Million cell updates/sec

Title: US-10-019-065A-1
Perfect score: 1231
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing First 45 summaries

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2: /cgn2_6/prodata/1/liaa/5B_COMB.pep:
3: /cgn2_5/prodata/1/liaa/5A_COMB.pep:
4: /cgn2_5/prodata/1/liaa/5B_COMB.pep:
5: /cgn2_6/prodata/1/liaa/PECTUS_COMB.pep:
6: /cgn2_6/prodata/1/liaa/backfiles1.pep:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	511.5	41.6	939	4	US-09-854-845-16	Sequence 16, AppI
2	511.5	41.6	954	4	US-09-854-845-14	Sequence 14, AppI
3	511.5	41.6	1034	4	US-09-854-845-6	Sequence 6, AppI
4	511.5	41.6	1049	4	US-09-854-845-2	Sequence 2, AppI
5	511.5	41.6	1078	4	US-09-854-845-8	Sequence 8, AppI
6	511.5	41.6	1093	4	US-09-854-845-4	Sequence 4, AppI
7	511.5	41.6	1136	4	US-09-854-845-12	Sequence 12, AppI
8	511.5	41.6	1151	4	US-09-854-845-10	Sequence 10, AppI
9	40.3	44.1	3	441	3	US-08-526-526
10	488.5	39.7	1170	4	US-08-313-288B-20	Sequence 20, AppI
11	488.5	39.7	1170	4	US-09-657-472-2	Sequence 2, AppI
12	478.5	38.9	239	5	PCT-US93-01652-1	Sequence 1, AppI
13	453	36.8	469	5	US-08-313-288B-15	Sequence 15, AppI
14	453	36.8	1172	1	US-08-313-288B-19	Sequence 19, AppI
15	417.5	33.9	788	2	US-08-918-914-4	Sequence 4, AppI
16	398	32.3	479	4	US-09-270-167-6823	Sequence 46823, A
17	360	29.2	218	3	US-08-985-126-1	Sequence 1, AppI
18	288.5	23.4	807	4	US-09-132-169-1	Sequence 1, AppI
19	288.5	23.4	807	4	US-09-640-173-186	Sequence 186, AppI
20	288.5	23.4	807	4	US-09-132-550-186	Sequence 186, AppI
21	288.5	23.4	807	4	US-09-825-294-186	Sequence 186, AppI
22	288.5	23.4	807	4	US-09-970-966-186	Sequence 186, AppI
23	23.4	23.4	787	4	US-09-825-294-207	Sequence 207, AppI
24	287.5	23.4	787	4	US-09-966-207	Sequence 207, AppI
25	287.5	23.4	807	1	US-07-862-021B-10	Sequence 10, AppI
26	287.5	23.4	807	1	US-08-313-288B-10	Sequence 10, AppI
27	287.5	23.4	807	4	US-09-132-769-3	Sequence 3, AppI

ALIGNMENTS

RESULT 1
US-09-854-845-16
; Sequence 16, Application US/09854845
; GENERAL INFORMATION:
; Patent No. 6750054
; APPLICANT: Walks, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and Polynucleotides Encod
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US 09/854, 845
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205, 274
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 16
; LENGTH: 939
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-854-845-16

Query Match 41.6%; Score 511.5; DB 4; Length 939;
Best Local Similarity 33.0%; Prod. No. 5.7e-16
Matches 94; Conservative 22; Mismatches 82; Indels 87; Gaps 3;

Qy 3 HGGFSQSWAARWACSYTCGKIQKRSRLCNQLPANGGKPCQGSQDLEMRC-QNKPCPVYDG 61
Db 467 NGATMPWSSWALCSTCGFQTRQRGSNPAHGRICVGSKSRERFCNTPCVPI 526
Qy 62 SWSEWSLWEECTRSGRGENOTRPTCTNPSPVHGGRCGEHAVEIMCNIRPCP---- 115
Db 527 FWASNGGSWSRKCSNNCGGMQSRERRACEN----GNSCLGCGEVEFKTCNPEGCCPEVRRNT 580
Qy 116 ----- 115
Db 581 PWTPWLPVNVTOGGARQEQRFRFTCRAPLADPHGLQFGRRRTETRTPADSGSCDTDAL 640
Qy 116 ----- 116
Db 641 VEDLIRSGSTSPTVSGWAAANGPWSSESRSRDCELGFYVRKSTCTNFBPRNGSLPCVGDAA 700
Qy 162 QMQVNENRNCP1HEKWAUTWASNSACSYSCGGEARQRGRGCSDPVP 206
Db 701 EYQDCNPQACPVRGAWSCTSHSPCSASSGGHYQRTSCTSPAP 745

RESULT 2

US-09-854-845-14

; Sequence 14, Application US/09854845

; Patent No. 6750054

; GENERAL INFORMATION:

; APPLICANT: Walké, D. Wade

; APPLICANT: Wang, Xiaoming

; APPLICANT: Scoville, John

; APPLICANT: Turner, C. Alexander Jr.

; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and Polynucleotides Encod

; FILE REFERENCE: LEX-0177-USA

; CURRENT APPLICATION NUMBER: US/09/854, 845

; CURRENT FILING DATE: 2001-05-14

; PRIOR APPLICATION NUMBER: US 60/205,274

; PRIORITY NUMBER: US 60/208,893

; PRIORITY FILING DATE: 2000-05-18

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: fastSEQ for Windows Version 4.0

; SEQ ID NO: 14

; LENGTH: 954

; ORGANISM: homo sapiens

US-09-854-845-14

Query Match 41.6%; Score 511.5; DB 4; Length 954;

Best Local Similarity 33.0%; Pred. No. 6.3e-35;

Matches 94; Conservative 22; Mismatches 82; Indels 87; Gaps 3;

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US-09-854-845-6

Query Match 41.6%; Score 511.5; DB 4; Length 1034;

Best Local Similarity 33.0%; Pred. No. 6.3e-35;

Matches 94; Conservative 22; Mismatches 82; Indels 87; Gaps 3;

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RESULT 4

US-09-854-845-2

; Sequence 2, Application US/09854845

; Patent No. 6750054

; GENERAL INFORMATION:

; APPLICANT: Walké, D. Wade

; APPLICANT: Wang, Xiaoming

; APPLICANT: Scoville, John

; APPLICANT: Turner, C. Alexander Jr.

; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and Polynucleotides Encod

; FILE REFERENCE: LEX-0177-USA

; CURRENT APPLICATION NUMBER: US/09/854, 845

; CURRENT FILING DATE: 2001-05-14

; PRIORITY NUMBER: US 60/208,893

; PRIORITY FILING DATE: 2000-05-18

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 2

; LENGTH: 1049

; TYPE: PRT

; ORGANISM: homo sapiens

US-09-854-845-2

Query Match 41.6%; Score 511.5; DB 4; Length 1049;

Best Local Similarity 33.0%; Pred. No. 6.3e-35;

Matches 94; Conservative 22; Mismatches 82; Indels 87; Gaps 3;

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RESULT 3

US-09-854-845-6

; Sequence 3, Application US/09854845

; Patent No. 6750054

; GENERAL INFORMATION:

; APPLICANT: Walké, D. Wade

; APPLICANT: Wang, Xiaoming

; APPLICANT: Scoville, John

; APPLICANT: Turner, C. Alexander Jr.

; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and Polynucleotides Encod

; FILE REFERENCE: LEX-0177-USA

; CURRENT APPLICATION NUMBER: US/09/854, 845

; CURRENT FILING DATE: 2001-05-14

; PRIORITY NUMBER: US 60/205,274

; PRIORITY FILING DATE: 2000-05-18

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: fastSEQ for Windows Version 4.0

; SEQ ID NO: 6

; LENGTH: 1034

; TYPE: PRT

; ORGANISM: homo sapiens

US-09-854-845-6

Query Match 41.6%; Score 511.5; DB 4; Length 1034;

Best Local Similarity 33.0%; Pred. No. 6.3e-35;

Matches 94; Conservative 22; Mismatches 82; Indels 87; Gaps 3;

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! SEQ ID NO 4
! LENGTH: 1093

RESULT 8

US-08-854-845-10

/ Sequence 10, Application US/09854845

/ Parent No. 6750054

/ GENERAL INFORMATION:

/ APPLICANT: Walk, D. Wade

/ APPLICANT: Wang, Xiaoming

/ APPLICANT: Scoville, John

/ APPLICANT: Turner, C. Alexander Jr.

/ TITLE OF INVENTION: No. 6750054 Human Semaphorin Homologs and Polynucleotides Encod

/ FILE REFERENCE: LEX-0177 USA

/ CURRENT APPLICATION NUMBER: US/09/854-845

/ PRIOR APPLICATION NUMBER: US/00-05-14

/ PRIOR FILING DATE: 2000-05-18

/ PRIOR APPLICATION NUMBER: US 60/205,274

/ PRIOR FILING DATE: 2000-06-02

/ NUMBER OF SEQ ID NOS: 50

/ SOFTWARE: FastSEQ for Windows Version 4.0

/ SEQ ID NO 10

/ LENGTH: 1151

/ TYPE: PRT

/ ORGANISM: homo sapiens

US-09-854-845-10

Query Match 41.6%; Score 511.5; DB 4; Length 1151;

Best Local Similarity 33.0%; Prd: No. 7e-35; Indels 87; Gaps 3;

Matches 94; Conservative 22; Mismatches 82;

Qy 3 HGGFSQSAWRACTSVTCGKGIIQKRSRLCNCNQPLPANGGKPCQSDLEMNC-QNKPCPVDG 61

Db 664 NGATWPMSWALCSTCGFQRQRSSNPAPRHRGIVCKSRSRERFCENTTCPVPI 723

Qy 62 SWSSEWLMEETCTSGRGNQNTPTCTCNPSVHGGRCBGNAVEIMCNTRPCP-----115

Db 724 FWAWSMSKCSNCGGMOSRRACEN----GNSCLGCGEVPTCNPGCPEVRRNT 777

Qy 116 -----115

Db 778 PWTPLWPNVTQGGARQEQRFRCTPAPLADPHGLQFGRRTEETRTCBDAGSGCDTDL 837

Qy 116 -----VHAWSAWQPMGTCSSESGKGTQTRALCNPPAFGGSYCDGAET 161

Db 838 VEDLRSGSTSPHTVSGWANGPSSCSRDELGRVRXKTCTNDEPRNGGLPCVGDA 897

Qy 162 QMQVCNRNCPIHGKRNWATWMSACSYSCGGGARQORTRGCDPVP 206

Db 898 BYQDCNFOACPVRGANSWCWTSASCGGHHYQRTSRCSITSPAP 942

RESULT 9

US-08-854-526-3

/ Sequence 3, Application US/08985326

/ Patent No. 6380728

/ GENERAL INFORMATION:

/ APPLICANT: Mixon, James A

/ TITLE OF INVENTION: CARRIER-DNA COMPLEXES CONTAINING DNA

/ TITLE OF INVENTION: ENCODING ANTI-ANGIOTIC PEPTIDES AND THEIR USE IN GENE

/ NUMBER OF SEQUENCES: 43

/ CORRESPONDENCE ADDRESS:

/ STREET: Connally, Bove, Lodge, & Hutz

/ CITY: Wilmington, Delaware

/ STATE: Delaware

RESULT 10

US-08-313-288B-20

/ Sequence 20, Application US/08313288B

/ Patent No. 5750502

/ GENERAL INFORMATION:

/ APPLICANT: Jessell, Thomas M. and Avihu Klar

/ TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A

/ TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN

/ NUMBER OF SEQUENCES: 20

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: Cooper & Dunham LLP

/ STREET: 1185 Avenue of the Americas

/ CITY: New York

/ STATE: New USA

/ ZIP: 10036

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-POS-MS-DOS
 SOFTWARE: PatientIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/313,288B
 FILING DATE: January 5, 1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REGISTRATION NUMBER: 28,678
 REFERENCE DOCKET NUMBER: 40028-A-PCT-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 278-0400
 TELEX: (212) 391-0526
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1170 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-313-288B-20

Query Match 39.7%; Score 488.5; DB 1; Length 1170;
 Best Local Similarity 41.9%; Pred. No. 6e-33; Gaps 6;
 Matches 91; Conservative 26; Mismatches 73; Indels 27; Gaps 6;

Qy 5 GFSQWSAARRACSYTCGKGIIQKRSRLCNQPLPANGKPCQGSDEMRNCQNPKC---PVD 60
 Db 381 GWSWSEWTSCSCTSGGIIQKRSRCD ---SLNNRCEGSSVQTRTHIQECDKRKFQD 435

Qy 61 GSNSEWSSLWEECTRSCGRGNQTRTRCNPSVQHGRPCEGNAVELIMCNTRCPYHGW 120
 Db 436 GGSHWSPWSSCSVTGCGVTRIRLNNSPSQMNGKPCGEARETKKDACPINGW 495

Qy 121 SAWOPWGTSOSECGKTOTRARIQNPPARGSYCDGAETOMQVNERNPIHG---- 175
 Db 496 GPNSPWIDICSVTGGVQKRSRLCNNAAPQFEDCYGDVTEQINCKQDCPDGCLSNP 555

Qy 176 ----KWTW--ASW--SACSVSCGGGARQRTRGCS 203
 Db 556 CPAGVKCTSYPPDSWKCGACPPGSQNGIQ---CTD 588

RESULT 12

PCT-US93-01652-1
 ; Sequence 1, Application PC/TUS9301652
 ; GENERAL INFORMATION:
 ; APPLICANT: Bouck, Noel P.
 ; APPLICANT: Polverini, Peter J.
 ; APPLICANT: Good, Deborah J.
 ; APPLICANT: Prizer, William A.
 ; TITLE OF INVENTION: Method and Composition for
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fallon, Lungmus & Chestnut
 ; STREET: 100 South Wacker Drive, Suite 960
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606-4002
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US93/01652
 ; FILING DATE: 19930222
 ; CLASSIFICATION:
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/841,656
 ; FILING DATE: 24-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/464,369
 ; FILING DATE: 12-JAN-1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fentress, Susan B.
 ; REGISTRATION NUMBER: 31,327
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (312)-456-8000
 ; TELEFAX: (312)-456-7776
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 239 amino acids
 ; TYPE: AMINO ACID
 ; STRANDEDNESS: unknown
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: peptide
 ; PCT-US93-01652-1

Query Match 38.9%; Score 478.5; DB 5; Length 239;
 Best Local Similarity 46.9%; Pred. No. 8.1e-33;

TYPE: PRF
 ORGANISM: Homo sapiens

US-09-657-472-2

Matches 82; Conservative 22; Mismatches 62; Indels 9; Gaps 2; Db 256 VAGGNGPWPVSPCPVTCGLGGTMEQRTCNHPVQHGGPFCAGDATRTHICNTAVPCPV 315

Qy 5 GFSQSONAARRASVTGKGIIKRSRLCNQPLANGKPKCGSDLEMRNCONKPC---PVD 60 Qy 175 GKWWATWASWSAC-----SVSCG--GGARORTRGSCDP 204

Db 70 GWSPSEWNTSOSTSGNGQQRGSCD---SLNTRBEGGSVOTRTHIQEDRRKQD 124 Db 316 GEWDNSGEWSPTCIRANMRS1SCQE1PGQOSRGRTORGPP 353

RESULT 14
US-08-313-288B-19
Sequence 19, Application US/08313288B

GENERAL INFORMATION:
Patent No. 5750502
APPLICANT: Thomas M. and Avihu Klar
TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A NOVEL SECRETED PROTEIN, F-SPONDIN
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
ZIP: 10036
CITY: New York
COUNTRY: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,288B
FILING DATE: January 5, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 40028-A-PCT-US
REFERENCE/DOCKET NUMBER: 40028-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0526
TELEX:
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 1172 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-313-288B-19

Query Match 36.8%; Score 453; DB 1; Length 1172;
Best Local Similarity 40.4%; Pred. No. 5.7e-20;
Matches 80; Conservative 26; Mismatches 76; Indels 16; Gaps 3;

Qy 5 GFSQSONAARRASVTGKGIIKRSRLCNQPLANGKPKCGSDLEMRNCONKPCPV--D 60
Db 383 GWSWAETQSYTCGSGTQERSCDVTT----SNTCLGPISIQTACSLSKCDTRIRD 437

Qy 61 GSNSEWSWAEETRSGGGNQPTRTCNPSVQHGGPCEGNAVEIMCNRPCPVHGAW 120
Db 438 GGSHSWWSKSSSAYTGGNPIRILNSPVPQMGCKSGSGRETKACQGAPCIDGRW 497

Qy 121 SAVQPGTCSSECGKGTOARLNNPPAFGGSYCDGAETOMOVNERNCPHG---175
Db 498 SPSPSPWACTVTCAGGRERTRVCNSFPQYGGKACYDVOERQCNRSCPVDGLSNP 557

Qy 176 --KWATWASWSACSVSC 191
Db 558 CFBGAQCCSFDPGSWSCG 575

RESULT 15
US-08-918-914-4
Sequence 4, Application US/08918914

Matches 87 Local Similarity 39.9%; Pred. No. 2.2e-20;
Mismatches 22; Indels 91; Gaps 8;
ANTI-SENSE: NO
US-08-313-288B-15

Query Match 36.8%; Score 453; DB 1; Length 469;
Best Local Similarity 40.4%; Pred. No. 2.2e-20;
Matches 87; Conservative 22; Mismatches 91; Indels 18; Gaps 8;

Qy 4 GGFSONAARRASVTGKGIIKRSRLCNQPLANGKPKCGSDLEMRNCONKPC-CPVDS 62
Db 137 GGSGWGWEPSCVTSRKSRAPESPQRKPCPKGAYEQRCTGLPPCP 255

Qy 63 WSEWSWAEETSGGRG---NQTRTRCN--NPSVQHGGPCEGNAVEIMC-NIRCP
Db 196 WATWGPWTCPSCASCHGSPHEPEKTRSRKSAPESPQRKPCPKGAYEQRCTGLPPCP 255

Qy 116 VIGAWSAWQPWGTCSBSCGKGQTTRALCNAPPAPGGSYCDGASTQMVCNER-NCPRH 174

Patent No. 5876963
 GENERAL INFORMATION:
 APPLICANT: Mitchell, Peter
 APPLICANT: Hutchinson, Nancy
 APPLICANT: Lawton, Michael
 APPLICANT: Magna, Holly
 APPLICANT: Yocum, Sue
 APPLICANT: Murty, Lynn E.
 TITLE OF INVENTION: HUMAN NUCLEOTIDE PYROPHORYLASE
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Dr.
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/0/918,914
 FILING DATE: Filed Herewith
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE DOCKET NUMBER: PP-0369
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166
 TELEX:
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 788 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GenBank
 CLONE: 1070094
 US-08-918-914-4

Query Match 33.9%; Score 417.5; DB 2; Length 788;
 Best Local Similarity 39.0%; Pred. No. 3 6e-77;
 Matches 78; Conservative 20; Mismatches 79; Indels 23; Gaps 6;
 Qy 2 VHGGSFSRSAVRACSVTCKGKGIOKRSRLCNQPLPANGKPKCGSDLEMRCNQNKPCPVDG 61
 Db 454 VSGWHDSDWSTCSCTGDKASRRRECST-----NCQGADYETEPNLGPQ-- 503

Qy 62 SNSSEWSLWEETRSRGGRGNNOTTRTCNNPSVQHGRPCCEGAETELMCNTRPCPVGAW 121
 Db 504 TNSEWCENSTCSASCGSQERTRFH---LGTRCEGDXESEQCSAGBCP --EWS 555

Qy 122 AWQPGTSESSCGKGQTQTRARLCNNPPAEGSYCDGAETMQVCNERNCPIHGRNATWA 181
 Db 556 QWDWGQSVTCCQGVAVRQRTCLG--GVFGDHLQGSPKTEQRACDGGPCSL--WSPWQ 610

Qy 182 SWSACSVSGGARQRTGCG 201
 Db 611 EWSTCSASOGSMKRRQVC 630



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OM protein - protein search, using sw model

Run on: November 17, 2004, 15:52:32 ; Search time 140 Seconds
 (without alignments)
 526.132 Million cell updates/sec

Title: US-10-019-065A-1
 Perfect score: 1231
 Sequence: QVHGGFESQWSAHRACSYTCG.....SCGGGARQRTRGCSDDPVQY 208

Scoring table: BLOSUM62
 Gapext 0.0 , Gapext 0.5

Searched: 1570615 seqs, 35412592 residues

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing First 45 summaries

Database : Published Applications AA:
 1: /cgn2_6/_prodatal/2/_pubpaas/US07_PUBCOMB.pep:
 2: /cgn2_6/_prodatal/2/_pubpaas/PCT_NEW_PUB.pep:
 3: /cgn2_6/_prodatal/2/_pubpaas/US06_PUBCOMB.pep:
 4: /cgn2_6/_prodatal/2/_pubpaas/US06_PUBCOMB.pep:
 5: /cgn2_6/_prodatal/2/_pubpaas/US07_PUBCOMB.pep:
 6: /cgn2_6/_prodatal/2/_pubpaas/US08_PUBCOMB.pep:
 7: /cgn2_6/_prodatal/2/_pubpaas/US08_PUBCOMB.pep:
 8: /cgn2_6/_prodatal/2/_pubpaas/US08_PUBCOMB.pep:
 9: /cgn2_6/_prodatal/2/_pubpaas/US09_PUBCOMB.pep:
 10: /cgn2_6/_prodatal/2/_pubpaas/US10_PUBCOMB.pep:
 11: /cgn2_6/_prodatal/2/_pubpaas/US09_PUBCOMB.pep:
 12: /cgn2_6/_prodatal/2/_pubpaas/US09_NEW_PUB.pep:
 13: /cgn2_6/_prodatal/2/_pubpaas/US10A_PUBCOMB.pep:
 14: /cgn2_6/_prodatal/2/_pubpaas/US10B_PUBCOMB.pep:
 15: /cgn2_6/_prodatal/2/_pubpaas/US10C_PUBCOMB.pep:
 16: /cgn2_6/_prodatal/2/_pubpaas/US10D_PUBCOMB.pep:
 17: /cgn2_6/_prodatal/2/_pubpaas/US10_NEW_PUB.pep:
 18: /cgn2_6/_prodatal/2/_pubpaas/US11_NEW_PUB.pep:
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 20: /cgn2_6/_prodatal/2/_pubpaas/US60_PUBCOMB.pep:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1
 US-10-019-065A-1
 ; Sequence 1, Application US/10019065A
 ; Publication No. US20040188501A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bayer Corporation
 ; TITLE OF INVENTION: Protein Having Activity As An Angiogenesis Modulator
 ; FILE REFERENCE: MSB-7265-PCT
 ; CURRENT APPLICATION NUMBER: US/10/019-065A
 ; CURRENT FILING DATE: 2002-08-30
 ; PRIORITY APPLICATION NUMBER: US 60/266,300
 ; PRIORITY FILING DATE: 2000-03-31
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; LENGTH: 208
 ; US-10-019-065A-1

Query Match 100.0%; Score 1231; DB 15; Length 208;
 Best Local Similarity 100.0%; Pred. No. 7.6e-93; Mismatches 0; Indels 0; Gaps 0;

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1231	100.0	208	15 US-10-019-065A-1	Sequence 1, Appli
2	1231	100.0	707	15 US-10-019-065A-1	Sequence 18, Appli
3	1231	100.0	1336	15 US-10-019-065A-33	Sequence 33, Appli
4	1231	100.0	1902	14 US-10-014-153-88	Sequence 88, Appli
5	1231	100.0	3645	14 US-10-120-801-73	Sequence 73, Appli
6	1231	100.0	5635	15 US-10-051-168-78	Sequence 78, Appli
7	1231	100.0	5636	14 US-10-032-159-128	Sequence 128, Appli
8	1231	100.0	5636	14 US-10-120-801-72	Sequence 72, Appli
9	1231	100.0	5636	14 US-10-023-634-93	Sequence 93, Appli
10	1231	100.0	5636	16 US-10-408-765A-1895	Sequence 1895, Appli
11	1230	99.9	2572	14 US-TUTT-153-86	Sequence 67, Appli
12	1230	99.9	2673	14 US-10-032-180-76	Sequence 76, Appli
13	1230	99.9	3645	14 US-10-032-189-127	Sequence 127, Appli

RESULT 3

```

Qy 181 ASWSACSVSCGGGARQRTGCGSDPVPQY 2 08
Db 181 ASWSACSVSCGGGARQRTGCGSDPVPQY 2 08

Query Match 100.0%; Score 1231; DB 15;
Best Local Similarity 100.0%; Pred. No. 4..2e-92;
Matches 208; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

Qy 1 QVHGGFSQWAVRACSVTGGTQKRSRLCNQPLANGKPCOGSDLEMNCQNKPCPVD 60
Db 471 QVHGGFSQWAVRACSVTGGTQKRSRLCNQPLANGKPCOGSDLEMNCQNKPCPVD 530

Qy 1 QVHGGFSQWAVRACSVTGGTQKRSRLCNQPLANGKPCOGSDLEMNCQNKPCPVD 60
Db 531 GSSEWSLWEBCTSGRGNQTRTCNNPSVQHGRPCGNAVEIMCNRPCPVHGAN 120
Db 531 GSSEWSLWEBCTSGRGNQTRTCNNPSVQHGRPCGNAVEIMCNRPCPVHGAN 590

Qy 121 SAWQFWGTCSESCCKGTCQTRARLCNNPPAFCGSYCDGAETOMQVCNERNCPTHGKWTW 180
Db 774 SAWQFWGTCSESCCKGTCQTRARLCNNPPAFCGSYCDGAETOMQVCNERNCPTHGKWTW 833

Qy 181 ASWSACSVSCGGGARQRTGCGSDPVPQY 208
Db 834 ASWSACSVSCGGGARQRTGCGSDPVPQY 861

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RESULT 4

```

US-10-114-153-88
Sequence 88, Application US/10114153
Publication No. US20030185815A1
GENERAL INFORMATION:
APPLICANT: Padigaru, Muralidhara
APPLICANT: Sheroy, Suresh
APPLICANT: Kekuda, Rameesh
APPLICANT: Rastelli, Luca
APPLICANT: Mezes, Peter
APPLICANT: Smithson, Glennnda
APPLICANT: Guo, Xiaojia
APPLICANT: Gerlach, Valerie
APPLICANT: Bozdog, Ferenc
APPLICANT: Li, Li
APPLICANT: Zerhusen, Bryan
APPLICANT: Tchernev, Velizar
APPLICANT: Gangoli, Esha
APPLICANT: Spytel, Kimberly
APPLICANT: Malyanjar, Uriel
APPLICANT: Parturajan, Meera
APPLICANT: Miller, Charles
APPLICANT: Taupier, Raymond J. Jr.
APPLICANT: Heyes, Melvyn
APPLICANT: Ju, Jingfang
APPLICANT: Peyman, John
APPLICANT: Catterton, Blina
APPLICANT: MacDougall, John
APPLICANT: Edinger, Shlomit
APPLICANT: Stone, David
APPLICANT: Matz, Ann
APPLICANT: TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES, NUCLEIC ACID
APPLICANT: TITLE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE
FILE REFERENCE: 21402-322A
CURRENT APPLICATION NUMBER: US/10/114-153
PRIORITY APPLICATION NUMBER: 60/281086
PRIORITY FILING DATE: 2002-08-06
PRIORITY APPLICATION NUMBER: 60/281966
PRIORITY FILING DATE: 2001-04-05
PRIORITY APPLICATION NUMBER: 60/282020
PRIORITY FILING DATE: 2001-04-06
PRIORITY APPLICATION NUMBER: 60/282910
PRIORITY FILING DATE: 2001-04-10
PRIORITY APPLICATION NUMBER: 60/283512
PRIORITY FILING DATE: 2001-04-12
PRIORITY APPLICATION NUMBER: 60/283444
PRIORITY FILING DATE: 2001-04-12
PRIORITY APPLICATION NUMBER: 60/283657

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RESULT 2

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US-10-138-588-18
Sequence 18, Application US/10138588
Publication No. US20040018594A1
GENERAL INFORMATION:
APPLICANT: Alsbrook, et al.
TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES, NUCLEAR ACI
FILE REFERENCE: 21402-347A
CURRENT APPLICATION NUMBER: US/10/138,588
PRIORITY APPLICATION NUMBER: 60/288,395
PRIOR FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: 60/308,901
PRIOR FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: 60/313,388
PRIOR FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/324,757
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 60/288,900
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 203
SEQ ID NO 18
LENGTH: 707
TYPE: PRT
ORGANISM: Homo sapiens
US-10-138-588-18

Query Match 100.0%; Score 1231; DB 15;
Best Local Similarity 100.0%; Pred. No. 2.3e-92;
Matches 208; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

Qy 1 QVHGGFSQWAVRACSVTGGTQKRSRLCNQPLANGKPCOGSDLEMNCQNKPCPVD 60
Db 471 QVHGGFSQWAVRACSVTGGTQKRSRLCNQPLANGKPCOGSDLEMNCQNKPCPVD 530

Qy 1 QVHGGFSQWAVRACSVTGGTQKRSRLCNQPLANGKPCOGSDLEMNCQNKPCPVD 60
Db 531 GSSEWSLWEBCTSGRGNQTRTCNNPSVQHGRPCGNAVEIMCNRPCPVHGAN 120
Db 531 GSSEWSLWEBCTSGRGNQTRTCNNPSVQHGRPCGNAVEIMCNRPCPVHGAN 590

Qy 121 SAWQFWGTCSESCCKGTCQTRARLCNNPPAFCGSYCDGAETOMQVCNERNCPTHGKWTW 180
Db 591 SAWQFWGTCSESCCKGTCQTRARLCNNPPAFCGSYCDGAETOMQVCNERNCPTHGKWTW 650

Qy 181 ASWSACSVSCGGGARQRTGCGSDPVPQY 208
Db 651 ASWSACSVSCGGGARQRTGCGSDPVPQY 678

```

RESULT 3

```

US-10-019-065A-33
Sequence 33, Application US/10019065A
Publication No. US2004000650A1
GENERAL INFORMATION:
APPLICANT: Bayer Corporation
TITLE OF INVENTION: Protein Having Activity As An Angiogenesis Modulator
FILE REFERENCE: MSB-7265-PT
CURRENT APPLICATION NUMBER: US/10/019,065A
CURRENT FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: US 60/266,300
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.1
SEQ ID NO 33
LENGTH: 1336
TYPE: PRT
ORGANISM: Homo sapiens
US-10-019-065A-33

```

PRIOR FILING DATE: 2001-04-13
 PRIOR APPLICATION NUMBER: 60/283710
 PRIOR FILING DATE: 2001-04-13
 PRIOR APPLICATION NUMBER: 60/283678
 PRIOR FILING DATE: 2001-04-13
 PRIOR APPLICATION NUMBER: 60/284234
 PRIOR FILING DATE: 2001-04-17
 Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 251
 SEQ ID NO: 88
 LENGTH: 1902
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-114-153-88

Query Match Score 1231; DB 14; Length 1902;
 Best Local Similarity 100.0%; Pred. No. 5.9e-32;
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVHGGFSONSAWRAGSVTCGKGIQRSLRLCNQPLPANGKPCOGSDLEMNCNCONKPCPVYD 60
 Db 911 QVHGGFSONSAWRAGSVTCGKGIQRSLRLCNQPLPANGKPCOGSDLEMNCNCONKPCPVYD 60
 Qy 61 GSWEWSLWEBCTRSRGNGNQTRTRCNPSVQHGRPCPEGADEVIMCNRCPVHGW 120
 Db 971 GSWEWSLWEBCTRSRGNGNQTRTRCNPSVQHGRPCPEGADEVIMCNRCPVHGW 120
 Qy 121 SAQWPWGTCSSESCGKGQTQTRALCNPPAFGSSYCDGAETOMQVCNERCPIHGKWTW 180
 Db 1031 SAQWPWGTCSSESCGKGQTQTRALCNPPAFGSSYCDGAETOMQVCNERCPIHGKWTW 180
 Qy 181 ASWSACSVSGGGARQRTGCSDPVPOY 208
 Db 1091 ASWSACSVSGGGARQRTGCSDPVPOY 1118

RESULT 5
 US-10-120-801-73
 Sequence 73, Application US/10120801
 Publication No. US20030203843A1
 GENERAL INFORMATION:
 APPLICANT: Pena, Carol
 APPLICANT: Guo, Xiaojia
 APPLICANT: Shinkarek, Richard
 APPLICANT: Padigaru, Muralidhara
 APPLICANT: Kekuda, Ramesh
 APPLICANT: Spytek, Kimberly
 APPLICANT: Meiraban, Fuad
 APPLICANT: Topper, James N.
 APPLICANT: Malyanikar, Uriel
 APPLICANT: Wasserman, Scott
 APPLICANT: Boinger, Shlomit
 APPLICANT: Smithson, Glennanda
 APPLICANT: Gunther, Erik
 APPLICANT: Komives, Lazzlo
 TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
 FILE REFERENCE: 21402-34-0
 CURRENT FILING DATE: 2002-04-11
 PRIOR APPLICATION NUMBER: 60/285748
 PRIOR FILING DATE: 2001-04-23
 PRIOR APPLICATION NUMBER: 60/286068
 PRIOR FILING DATE: 2001-04-24
 PRIOR APPLICATION NUMBER: 60/286292
 PRIOR FILING DATE: 2001-04-25
 PRIOR APPLICATION NUMBER: 60/288334
 PRIOR FILING DATE: 2001-05-03
 PRIOR APPLICATION NUMBER: 60/291241
 PRIOR FILING DATE: 2001-05-16
 PRIOR APPLICATION NUMBER: 60/322284
 PRIOR FILING DATE: 2001-09-14
 PRIOR APPLICATION NUMBER: 60/285609
 PRIOR FILING DATE: 2001-04-20

; NUMBER OF SEQ ID NOS: 155 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 73 ;
 ; LENGTH: 3645 ;
 ; TYPE: PRT ;
 ; ORGANISM: human ;
 US-10-120-801-73

Query Match Score 1231; DB 14; Length 3645;
 Best Local Similarity 100.0%; Pred. No. 1.1e-91; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVHGGFSONSAWRAGSVTCGKGIQRSLRLCNQPLPANGKPCOGSDLEMNCNCONKPCPVYD 60
 Db 2537 QVHGGFSONSAWRAGSVTCGKGIQRSLRLCNQPLPANGKPCOGSDLEMNCNCONKPCPVYD 2596
 Qy 61 GSWEWSLWEBCTRSRGNGNQTRTRCNPSVQHGRPCPEGADEVIMCNRCPVHGW 120
 Db 2597 GSWEWSLWEBCTRSRGNGNQTRTRCNPSVQHGRPCPEGADEVIMCNRCPVHGW 2656
 Qy 121 SAQWPWGTCSSESCGKGQTQTRALCNPPAFGSSYCDGAETOMQVCNERCPIHGKWTW 180
 Db 2657 SAQWPWGTCSSESCGKGQTQTRALCNPPAFGSSYCDGAETOMQVCNERCPIHGKWTW 2716
 Qy 181 ASWSACSVSGGGARQRTGCSDPVPOY 208
 Db 2717 ASWSACSVSGGGARQRTGCSDPVPOY 2744

RESULT 6
 US-10-451-168-78
 Sequence 78, Application US/10451168
 Publication No. US20040091969A1
 GENERAL INFORMATION:
 APPLICANT: SMITHLINE BEACHEM CORPORATION ;
 APPLICANT: GLAXO GROUP LIMITED ;
 TITLE OF INVENTION: NOVEL COMPOUNDS ;
 FILE REFERENCE: GP50039 ;
 CURRENT APPLICATION NUMBER: US/10/451,168 ;
 CURRENT FILING DATE: 2003-11-12 ;
 PRIOR APPLICATION NUMBER: PCT/US01/49232 ;
 PRIOR FILING DATE: 2000-12-17 ;
 PRIOR APPLICATION NUMBER: 60/256,710 ;
 PRIOR FILING DATE: 2000-12-19 ;
 PRIOR APPLICATION NUMBER: 60/257,048 ;
 PRIOR FILING DATE: 2000-12-20 ;
 PRIOR APPLICATION NUMBER: 60/260,482 ;
 PRIOR FILING DATE: 2001-01-09 ;
 PRIOR APPLICATION NUMBER: 60/264,922 ;
 PRIOR FILING DATE: 2001-01-30 ;
 PRIOR APPLICATION NUMBER: 60/266,797 ;
 PRIOR FILING DATE: 2001-02-06 ;
 NUMBER OF SEQ ID NOS: 110 ;
 SOFTWARE: FastSeq for Windows Version 4.0 ;
 SEQ ID NO: 78

Query Match Score 1231; DB 15; Length 5635;
 Best Local Similarity 100.0%; Pred. No. 1.e-91; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVHGGFSONSAWRAGSVTCGKGIQRSLRLCNQPLPANGKPCOGSDLEMNCNCONKPCPVYD 60

RESULT 7
 US-10-032-189-128
 ; Sequence 128, Application US/10032189
 ; Publication No. US20030170630A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alsobrook II, John P
 ; APPLICANT: Tchernay, Velizar T
 ; APPLICANT: Liu, Xiohong
 ; APPLICANT: Spytek, Kimberly A
 ; APPLICANT: Zerhusen, Bryan D
 ; APPLICANT: Patterson, Meera
 ; APPLICANT: Gross, William M
 ; APPLICANT: Lepley, Denise M
 ; APPLICANT: Burgess, Catharine E
 ; APPLICANT: Shimkets, Richard A
 ; APPLICANT: Grosse, William M
 ; APPLICANT: Szekeres, Edward S
 ; APPLICANT: Vernet, Corine A.M.
 ; APPLICANT: Li, Li
 ; APPLICANT: Cashan, Stacie J
 ; APPLICANT: Boldog, Ferenc L
 ; APPLICANT: Gorman, Linda
 ; APPLICANT: Ganguli, Esha A
 ; APPLICANT: Fernandes, Elma R
 ; APPLICANT: Rieger, Daniel K
 ; APPLICANT: Edinger, Shlomit R
 ; APPLICANT: Gunther, Erik
 ; APPLICANT: Millet, Isabelle
 ; APPLICANT: Sciore, Paul
 ; APPLICANT: Elterman, Karen
 ; APPLICANT: Machougal, John R
 ; APPLICANT: Smithson, Glenna
 ; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
 ; FILE REFERENCE: 21402-228
 ; CURRENT APPLICATION NUMBER: US/10/032-189
 ; CURRENT FILING DATE: 2001-12-21
 ; PRIOR APPLICATION NUMBER: 60/257,495
 ; PRIOR FILING DATE: 2000-12-21
 ; PRIOR APPLICATION NUMBER: 60/258,171
 ; PRIOR FILING DATE: 2000-12-20
 ; PRIOR APPLICATION NUMBER: 60/269,940
 ; PRIOR FILING DATE: 2001-02-20
 ; PRIOR APPLICATION NUMBER: 60/274,192
 ; PRIOR FILING DATE: 2001-03-08
 ; PRIOR APPLICATION NUMBER: 60/277,826
 ; PRIOR FILING DATE: 2001-03-22
 ; PRIOR APPLICATION NUMBER: 60/279,840
 ; PRIOR FILING DATE: 2001-03-29
 ; PRIOR APPLICATION NUMBER: 60/282,981
 ; PRIOR FILING DATE: 2001-04-11
 ; PRIOR APPLICATION NUMBER: 60/283,656
 ; PRIOR FILING DATE: 2001-04-13
 ; PRIOR APPLICATION NUMBER: 60/299,247
 ; PRIOR FILING DATE: 2001-07-31
 ; PRIOR APPLICATION NUMBER: 60/311,754
 ; PRIOR FILING DATE: 2001-08-17
 ; PRIOR APPLICATION NUMBER: 60/313,331
 ; PRIOR FILING DATE: 2001-08-17

RESULT 8
 US-10-120-801-72
 ; Sequence 72, Application US/10120801
 ; Publication No. US20030203843A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Guo, Xiaojia
 ; APPLICANT: Shimkets, Richard
 ; APPLICANT: Padigaru, Muralidhara
 ; APPLICANT: Kekuda, Ramesh
 ; APPLICANT: Spytek, Kimberly
 ; APPLICANT: Mehraban, Foad
 ; APPLICANT: Topper, James N.
 ; APPLICANT: Malyankar, Uriel
 ; APPLICANT: Wasserman, Scott
 ; APPLICANT: Edinger, Shlomit
 ; APPLICANT: Smithson, Glenna
 ; APPLICANT: Gunther, Erik
 ; APPLICANT: Komives, Laszlo
 ; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
 ; FILE REFERENCE: 21402-340
 ; CURRENT FILING DATE: 2002-04-11
 ; PRIOR APPLICATION NUMBER: 60/285748
 ; PRIOR FILING DATE: 2001-04-23
 ; PRIOR APPLICATION NUMBER: 60/286068
 ; PRIOR FILING DATE: 2001-04-24
 ; PRIOR APPLICATION NUMBER: 60/286292
 ; PRIOR FILING DATE: 2001-04-25
 ; PRIOR APPLICATION NUMBER: 60/288334
 ; PRIOR FILING DATE: 2001-05-03
 ; PRIOR APPLICATION NUMBER: 60/291241

PRIOR FILING DATE: 2001-05-16
 PRIOR APPLICATION NUMBER: 60/322284
 PRIOR FILING DATE: 2001-09-14
 PRIOR APPLICATION NUMBER: 60/285609
 PRIOR FILING DATE: 2001-04-20
 NUMBER OF SEQ ID Nos: 155
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 72
 LENGTH: 5636
 TYPE: PRT
 ORGANISM: human
 FEATURE:
 NAME/KEY: VARIANT
 LOCATION: (3003)
 OTHER INFORMATION: Wherein Xaa is any amino acid.
 FEATURE:
 NAME/KEY: VARIANT
 LOCATION: (3041)
 OTHER INFORMATION: Wherein Xaa is any amino acid.
 FEATURE:
 NAME/KEY: VARIANT
 LOCATION: (3367)
 OTHER INFORMATION: Wherein Xaa is any amino acid.
 US-10-120-801-72

Query Match 100.0%; Score 1231; DB 14; Length 5636;
 Best Local Similarity 100.0%; Pred. No. 1.6e-91; Mismatches 0; Indels 0; Gaps 0;
 Matches 208; Conservative 0; Type: PRT
 Organism: Homo sapiens
 Feature: Variant
 Name/Key: Variant
 Location: (3003)
 Other Information: Wherin Xaa is any amino acid as defined in the
 specification.
 Feature:
 Name/Key: Variant
 Location: (3041)
 Other Information: Wherin Xaa is any amino acid as defined in the
 specification.
 Feature:
 Name/Key: Variant
 Location: (3367)
 Other Information: Wherin Xaa is any amino acid as defined in the
 specification.

US-10-023-634-93

RESULT 9
 US-10-023-634-93
 Sequence 93, Application US/10023634
 Publication No. US200302163891
 GENERAL INFORMATION:
 APPLICANT: Shmikets, Richard A
 APPLICANT: Colman, Steven D
 APPLICANT: Spytek, Kimberly A
 APPLICANT: Ballinger, Robert A
 APPLICANT: Guo, Xiaojia
 APPLICANT: Tcherny, Velizar T
 APPLICANT: Shenoy, Suresh G
 APPLICANT: Li, Li
 APPLICANT: Elerman, Karen
 APPLICANT: Zerhusen, Bryan D
 APPLICANT: Patturajan, Meera
 APPLICANT: Casman, Stacie J
 APPLICANT: Boldog, Ferenc
 APPLICANT: Burgess, Catherine E
 APPLICANT: Edinger, Shlomit R
 APPLICANT: Gangoli, Esha A
 APPLICANT: Malyankar, Uriel M
 APPLICANT: Gunther, Erik
 APPLICANT: Smitsmon, Glennanda
 APPLICANT: Millet, Isabelle
 APPLICANT: Gerlach, Valerie

Query Match 100.0%; Score 1231; DB 14; Length 5636;
 Best Local Similarity 100.0%; Pred. No. 1.6e-91; Mismatches 0; Indels 0; Gaps 0;
 Matches 208; Conservative 0; Type: PRT
 Organism: Homo sapiens
 Feature: Variant
 Name/Key: Variant
 Location: (3003)
 Other Information: Wherin Xaa is any amino acid as defined in the
 specification.
 Feature:
 Name/Key: Variant
 Location: (3041)
 Other Information: Wherin Xaa is any amino acid as defined in the
 specification.
 Feature:
 Name/Key: Variant
 Location: (3367)
 Other Information: Wherin Xaa is any amino acid as defined in the
 specification.

US-10-023-634-93

RESULT 10
 US-10-408-765A-1895
 Sequence 1895, Application US/10408765A
 Publication No. US20040101874A1
 GENERAL INFORMATION:
 APPLICANT: Ghosh, Soumitra S.

; APPLICANT: Fahy, Eoin D.
 ; APPLICANT: Zhang, Bing
 ; APPLICANT: Gibson, Bradford W.
 ; APPLICANT: Taylor, Steven W.
 ; APPLICANT: Glenn, Gary M.
 ; APPLICANT: Warnock, Dale E.
 ; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
 ; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
 ; FILE REFERENCE: 600088-465
 ; CURRENT APPLICATION NUMBER: US/10/408,765A
 ; CURRENT FILING DATE: 2003-04-04
 ; NUMBER OF SEQ ID NOS: 3077
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 1895
 ; LENGTH: 5636
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE: VARIANT
 ; NAME/KEY: VARIANT
 ; LOCATION: 3003, 3041, 3367
 ; OTHER INFORMATION: Xaa = Any Amino Acid
 US-10-408-765A-1895

Query Match 100.0%; Score 1231; DB 16; Length 5636;
 Best Local Similarity 100.0%; Pred. No. 1..6..91;
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVHGGFSOKSAVACSVTCKGKIQKRSPLCNQPLPANGKPCQGSDELMRNCQNKECPVD 60
 Db 4528 QVHGGFSOKSAVACSVTCKGKIQKRSPLCNQPLPANGKPCQGSDELMRNCQNKECPVD 4587

Qy 61 GSNSEWSLMECTRSGRGNQTRTRTCNNPSYQHGRPCBNAVELIMCNTRCPVHGAW 120
 Db 4588 GSNSEWSLMECTRSGRGNQTRTRTCNNPSYQHGRPCBNAVELIMCNTRCPVHGAW 4647

Qy 121 SANOPWGTSSESCKGQTQTRARLCNNPPAFGGSYCDGAETOMQVCNERNPIHGKWTW 180
 Db 4648 SANOPWGTCSESCKGQTQTRARLCNNPPAFGGSYCDGAETOMQVCNERNPIHGKWTW 4707

Qy 181 ASWSACSVSCGGARQRTGCSDPVPQY 208
 Db 4708 ASWSACSVSCGGARQRTGCSDPVPQY 4735

RESULT 11
 ; Sequence 86, Application US/10114153
 ; Publication No. US20030185815A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pasigaru, Muralidhara
 ; APPLICANT: Shenoy, Suresh
 ; APPLICANT: Kekuda, Ramesh
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: Mezes, Peter
 ; APPLICANT: Smithson, Glenna
 ; APPLICANT: Guo, Xiaojia
 ; APPLICANT: Gerlach, Valerie
 ; APPLICANT: Casman, Stacie
 ; APPLICANT: Boldog, Ferenc
 ; APPLICANT: Li, Li
 ; APPLICANT: Zerhusen, Bryan
 ; APPLICANT: Tchernev, Velizar
 ; APPLICANT: Gangoli, Esha
 ; APPLICANT: Vernet, Corinne
 ; APPLICANT: Spytel, Kimberly
 ; APPLICANT: Malyankar, Uriel
 ; APPLICANT: Patturajan, Meera
 ; APPLICANT: Miller, Charles
 ; APPLICANT: Taupier, Raymond J. Jr.
 ; APPLICANT: Heyes, Melvyn
 ; APPLICANT: Ju, Jingfang
 ; APPLICANT: Peiman, John
 ; APPLICANT: Catterton, Elina

; APPLICANT: MacDougall, John
 ; APPLICANT: Edinger, Shlomit
 ; APPLICANT: Stone, David
 ; APPLICANT: Mazur, Ann
 ; TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTAGENS, AND METHODS OF USE
 ; TITLE OF INVENTION: ENCODING THE ANTAGENS, AND METHODS OF USE
 ; CURRENT APPLICATION NUMBER: US/10/114,153
 ; CURRENT FILING DATE: 2002-08-16
 ; PRIOR APPLICATION NUMBER: 60/281086
 ; PRIOR FILING DATE: 2001-04-03
 ; PRIOR APPLICATION NUMBER: 60/281906
 ; PRIOR FILING DATE: 2001-04-05
 ; PRIOR APPLICATION NUMBER: 60/282020
 ; PRIOR FILING DATE: 2001-04-06
 ; PRIOR APPLICATION NUMBER: 60/282930
 ; PRIOR FILING DATE: 2001-04-10
 ; PRIOR APPLICATION NUMBER: 60/283512
 ; PRIOR FILING DATE: 2001-04-12
 ; PRIOR APPLICATION NUMBER: 60/283444
 ; PRIOR FILING DATE: 2001-04-12
 ; PRIOR APPLICATION NUMBER: 60/284234
 ; PRIOR FILING DATE: 2001-04-13
 ; PRIOR APPLICATION NUMBER: 60/284424
 ; PRIOR FILING DATE: 2001-04-17
 ; PRIOR APPLICATION NUMBER: 60/284657
 ; PRIOR APPLICATION NUMBER: 60/2843710
 ; PRIOR FILING DATE: 2001-04-13
 ; PRIOR APPLICATION NUMBER: 60/283678
 ; PRIOR FILING DATE: 2001-04-13
 ; PRIOR APPLICATION NUMBER: 60/284234
 ; PRIOR FILING DATE: 2001-04-17
 ; PRIOR APPLICATION NUMBER: 60/284657
 ; NUMBER OF SEQ ID NOS: 251
 ; SEQ ID NO: 86
 ; LENGTH: 2572
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-114-153-86

Query Match 99.9%; Score 1230; DB 14; Length 2572;
 Best Local Similarity 99.5%; Prod. No. 9..e-92%;
 Matches 207; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVHGGFSOKSAVACSVTCKGKIQKRSPLCNQPLPANGKPCQGSDELMRNCQNKECPVD 60
 Db 1581 QVHGGFSOKSAVACSVTCKGKIQKRSPLCNQPLPANGKPCQGSDELMRNCQNKECPVD 1640

Qy 61 GSNSEWSLMECTRSGRGNQTRTRTCNNPSYQHGRPCBNAVELIMCNTRCPVHGAW 120
 Db 1641 GSNSEWSLMECTRSGRGNQTRTRTCNNPSYQHGRPCBNAVELIMCNTRCPVHGAW 1700

Qy 121 SANOPWGTCSESCKGQTQTRARLCNNPPAFGGSYCDGAETOMQVCNERNPIHGKWTW 180
 Db 1701 SANOPWGTCSESCKGQTQTRARLCNNPPAFGGSYCDGAETOMQVCNERNPIHGKWTW 1760

Qy 181 ASWSACSVSCGGARQRTGCSDPVPQY 208
 Db 1761 ASWSACSVSCGGARQRTGCSDPVPQY 1788

RESULT 12
 ; Sequence 76, Application US/101120801
 ; Publication No. US20030203843A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pera, Carol
 ; APPLICANT: Guo, Xiaojia
 ; APPLICANT: Shimkets, Richard
 ; APPLICANT: Padigaru, Ramesh
 ; APPLICANT: Kesuda, Ramesh
 ; APPLICANT: Spytel, Kimberly
 ; APPLICANT: Mehraban, Fuad
 ; APPLICANT: Topper, James N.
 ; APPLICANT: Malyankar, Uriel
 ; APPLICANT: Catterton, Elina

1 / APPLICANT: Edinger, Shlomit
 1 / APPLICANT: Smitsison, Glennda
 1 / APPLICANT: Gunther, Erik
 1 / APPLICANT: Karmuvics, Laszlo
 1 / TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
 1 / FILE REFERENCE: 214.02.340
 1 / CURRENT APPLICATION NUMBER: US 10/120, 801
 1 / CURRENT FILING DATE: 2002-04-11
 1 / PRIOR APPLICATION NUMBER: 60/288748
 1 / PRIOR FILING DATE: 2001-04-23
 1 / PRIOR APPLICATION NUMBER: 60/286668
 1 / PRIOR FILING DATE: 2001-04-24
 1 / PRIOR APPLICATION NUMBER: 60/286292
 1 / PRIOR FILING DATE: 2001-04-25
 1 / PRIOR APPLICATION NUMBER: 60/288334
 1 / PRIOR FILING DATE: 2001-04-26
 1 / PRIOR APPLICATION NUMBER: 60/291241
 1 / PRIOR FILING DATE: 2001-05-16
 1 / SEQ ID NO: 76
 1 / LENGTH: 2673
 1 / TYPE: PRT
 1 / ORGANISM: human
 1 / FEATURE:
 1 / NAME/KEY: VARIANT
 1 / LOCATION: (119)
 1 / OTHER INFORMATION: Wherein xaa is any amino acid.
 US-10-120-801-76

Query Match 99.9%; Score 1230; DB 14; Length 2673;
 Best Local Similarity 99.5%; Pred. No. 9.7e-92;
 Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVHGGFSSWAVRACSYTCKGKIQRSRLCNCNQPLPANGKPCQGSDELMRNQNPKCPVD 60
 Db 1565 QVHGGFSSWAVRACSYTCKGKIQRSRLCNCNQPLPANGKPCQGSDELMRNQNPKCPVD 1624
 Qy 61 GSWEWSLWEETRSQRGRNQTRTRCNPPSVQHGRPCQEGNAVELIMCNTRPCPVHGAW 120
 Db 1625 GSWEWSLWEETRSQRGRNQTRTRCNPPSVQHGRPCQEGNAVELIMCNTRPCPVHGAW 1684

Qy 121 SAQWPAGTCSESCKGKTQTRARLCNNPPAEGGSYCDGAETMQVNERNCPHGKWTW 180
 Db 1685 SAQWPAGTCSESCKGKTQTRARLCNNPPAEGGSYCDGAETMQVNERNCPHGKWTW 1744

Qy 181 ASWSACSVSCGGGARQTRGCSDPVPQY 208
 Db 1745 ASWSACSVSCGGGARQTRGCSDPVPQY 1772

RESULT 13
 US-10-032-189-127
 1 / Sequence 127, Application US/10032189
 1 / Publication No. US2003017063041
 1 / GENERAL INFORMATION
 1 / APPLICANT: Alsobrook II, John P
 1 / APPLICANT: Tcherny, Velizar T
 1 / APPLICANT: Liu, Xiaohong
 1 / APPLICANT: Sbytek, Kimberly A
 1 / APPLICANT: Zerhusen, Bryan D
 1 / APPLICANT: Patturajan, Meera
 1 / APPLICANT: Grosse, William M
 1 / APPLICANT: Lepley, Denise M
 1 / APPLICANT: Burgess, Catherine E
 1 / APPLICANT: Shimkets, Richard A
 1 / APPLICANT: Gross, William M
 1 / APPLICANT: Szekeles, Edward S
 1 / APPLICANT: Vernet, Corine A.M.

1 / APPLICANT: Li, Li
 1 / APPLICANT: Casman, Stacie J
 1 / APPLICANT: Boldog, Ferenc L
 1 / APPLICANT: Gorman, Linda
 1 / APPLICANT: Gangolfi, Esha A
 1 / APPLICANT: Fernandes, Elma R
 1 / APPLICANT: Rieger, Daniel X
 1 / APPLICANT: Edinger, Shlomit R
 1 / APPLICANT: Gunther, Erik
 1 / APPLICANT: Millet, Isabelle
 1 / APPLICANT: Sciore, Paul
 1 / APPLICANT: Ellerman, Karen
 1 / APPLICANT: Macdougall, John R
 1 / APPLICANT: Smithson, Glennda
 1 / TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
 1 / CURRENT APPLICATION NUMBER: US/10/032,189
 1 / CURRENT FILING DATE: 2001-12-21
 1 / FILE REFERENCE: 214.02-28
 1 / PRIOR APPLICATION NUMBER: 60/257,495
 1 / PRIOR FILING DATE: 2000-12-21
 1 / PRIOR APPLICATION NUMBER: 60/258,171
 1 / PRIOR FILING DATE: 2000-12-20
 1 / PRIOR APPLICATION NUMBER: 60/269,940
 1 / PRIOR FILING DATE: 2001-02-20
 1 / PRIOR APPLICATION NUMBER: 60/274,192
 1 / PRIOR FILING DATE: 2001-03-08
 1 / PRIOR APPLICATION NUMBER: 60/277,826
 1 / PRIOR FILING DATE: 2001-03-22
 1 / PRIOR APPLICATION NUMBER: 60/279,840
 1 / PRIOR FILING DATE: 2001-03-29
 1 / PRIOR APPLICATION NUMBER: 60/282,981
 1 / PRIOR FILING DATE: 2001-04-11
 1 / PRIOR APPLICATION NUMBER: 60/283,656
 1 / PRIOR FILING DATE: 2001-04-13
 1 / PRIOR APPLICATION NUMBER: 60/309,247
 1 / PRIOR FILING DATE: 2001-07-31
 1 / PRIOR APPLICATION NUMBER: 60/311,754
 1 / PRIOR FILING DATE: 2001-08-17
 1 / PRIOR APPLICATION NUMBER: 60/313,331
 1 / PRIOR FILING DATE: 2001-08-17
 1 / NUMBER OF SEQ ID NOS: 260
 1 / SOFTWARE: PatentIn Ver. 2.1
 1 / SEQ ID NO: 127
 1 / LENGTH: 3645
 1 / TYPE: PRT
 1 / ORGANISM: Homo sapiens
 US-10-032-189-127

Query Match 99.9%; Score 1230; DB 14; Length 3645;
 Best Local Similarity 99.5%; Pred. No. 1.3e-91;
 Matches 207; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVHGGFSSWAVRACSYTCKGKIQRSRLCNCNQPLPANGKPCQGSDELMRNQNPKCPVD 60
 Db 2537 QVHGGFSSWAVRACSYTCKGKIQRSRLCNCNQPLPANGKPCQGSDELMRNQNPKCPVD 2596

RESULT 14
 US-10-138-588-20
 1 / Sequence 20, Application US/10138588
 1 / Publication No. US20040018594A1

GENERAL INFORMATION:

APPLICANT: Alsobrook et al.

TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES, NUCLEIC ACI

TITLE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE

FILE REFERENCE: 214-02-347A

CURRENT APPLICATION NUMBER: US/10/138,588

CURRENT FILING DATE: 2002-05-01

PRIOR APPLICATION NUMBER: 60/288,395

PRIOR FILING DATE: 2001-05-03

PRIOR APPLICATION NUMBER: 60/308,901

PRIOR FILING DATE: 2001-07-31

PRIOR APPLICATION NUMBER: 60/313,388

PRIOR FILING DATE: 2001-08-17

PRIOR APPLICATION NUMBER: 60/324,757

PRIOR APPLICATION NUMBER: 60/288,900

PRIOR FILING DATE: 2001-05-04

NUMBER OF SEQ ID NOS: 203

SEQ ID NO 20

LENGTH: 4495

TYPE: PRT

ORGANISM: Homo sapiens

US-10-138-588-20

Query Match 99.9%; Score 1230; DB 15; Length 4495;

Best Local Similarity 99.5%; Prd. No. 1.6e-91;

Matches 207; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVHGGFSQNSAWACSVTGGKGIQTRSLCNPQPLANGKPCOGSDEMRNCQNKPCPVD 60

Db 3387 QVHGGFSQNSAWACSVTGGKGIQTRSLCNPQPLANGKPCOGSDEMRNCQNKPCPVD 3446

Qy 61 GSNSEWSLMECTRSCEGRNQTRTRTCNNPSYQHGRPCGNAEVIMCNIRCPVHGAW 120

Db 3447 GSNSEWSLWEETRSCEGRNQTRTRTCNNPSYQHGRPCGNAEVIMCNIRCPVHGAW 3505

Qy 121 SANQPWGTQESCGKGQTOTRARICLNNPPAFGSYCDGAETOMQVCNERNCPIHGWATW 180

Db 3507 SANQPWGTCSESCQKGQTOTRARICLNNPPAFGSYCDGAETOMQVCNERNCPIHGWATW 3566

Qy 181 ASMSACSVSCGGGARQTRGSDPVPQY 208

Db 3557 ASMSACSVSCGGGARQTRGSDPVPQY 3594

RESULT 15

US-10-019-065A-31

Sequence 31, Application US/10019065A

Publication No. US20040086501A1

GENERAL INFORMATION:

APPLICANT: Bayer Corporation

TITLE OF INVENTION: Protein Having Activity As An Angiogenesis Modulator

FILE REFERENCE: MSS-7265-PT

CURRENT APPLICATION NUMBER: US/10/019,065A

CURRENT FILING DATE: 2002-08-30

PRIOR APPLICATION NUMBER: US 60/266,300

PRIOR FILING DATE: 2000-03-31

NUMBER OF SEQ ID NOS: 34

SOFTWARE: PatentIn version 3.1

SEQ ID NO 31

LENGTH: 197

TYPE: PRT

ORGANISM: Homo sapiens

US-10-019-065A-31

Query Match 95.0%; Score 1169; DB 15; Length 197;

Best Local Similarity 100%; Prd. No. 8.3e-88;

Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 QMSAWRACSVTGGKGIQTRSLCNPQPLANGKPCOGSDEMRNCQNKPCPVDSSWENS 67

Db 1 QMSAWRACSVTGGKGIQTRSLCNPQPLANGKPCOGSDEMRNCQNKPCPVDSSWENS 60

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using sw model

OM protein - protein search, using sw model

Run on: November 17, 2004, 15:44:52 ; Search time 40 Seconds

(without alignments)

500.327 Million cell updates/sec

Title: US-10-019-065A-1

Perfect score: 1231

Sequence: 1 QVHGGFSONSAWRACSVTCG.....SCGGGARQRTRGCSDPVHQY 208

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_79;*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	522.5	42.4	1074	2	JCS928	seamphorin F precursor - human
2	519.5	42.2	1584	2	T0026	C;Species: Homo sapiens (man)
3	503.5	40.9	984	2	T00326	C;Date: 10-Apr-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
4	503.5	40.9	1522	2	T00028	R;Simmons, A.D.; Pueschel, A.W.; McPherson, J.D.; Overhauser, J.; Lovett, M.
5	492.5	40.0	1170	2	A04058	Biochem. Biophys. Res. Commun. 242, 683-691, 1998
6	488.5	39.8	1572	2	T0027	A;Title: Molecular cloning and mapping of human seamphorin F from the Cri-du-chat candid
7	488.5	39.7	1170	1	TSHP1	A;Reference number: JCS928; PMID:9812554; MID:104-9464278
8	474.5	38.5	437	2	S05478	A;Accession: JCS928
9	472.2	38.3	1444	2	A18856	A;Status: nucleic acid sequence not shown
10	466	37.9	1178	1	A39804	A;Molecule type: mRNA
11	453	36.8	1172	1	TSHP2	A;Residues: 1-1074 <SIM>
12	451	36.7	1172	2	A42587	A;Cross-references: UNIPROT:Q13591; GS:U52240; NID:977253; PIDN:AC09473.1; PMID:927725
13	449	36.5	469	1	S29126	A;Experimental source: brain
14	441	35.8	957	2	T15976	C;Comment: This protein disrupts normal brain development and leads to some of the featu
15	417.5	33.9	788	2	T25061	C;Genetics:
16	322.5	33.6	712	2	A45638	C;Superfamily: human seamphorin F; thrombospondin type 1 repeat homology
17	311	25.3	724	2	A48869	F;1-20/Domain: signal peptide<SIM>
18	304.5	24.7	206	2	A45517	F;50-533/Domain: seamphorin #status predicted <SEM>
19	296.5	24.1	803	2	A47723	F;840-896/Domain: thrombospondin type 1 repeat homology <TRH3>
20	287.5	23.4	807	2	A38152	F;971-993/Domain: transmembrane #status predicted <TRM>
21	276	22.4	2165	2	T21371	Query Match 95%保守性 Best Local Similarity 33.4% Matches 95/95 Score 522.5; DB 2; Length 1074;
22	262	21.3	1360	2	T3322	Best Local Similarity 33.1% Pred. No. 1e-31; Indels 87; Gaps 3;
23	257	20.9	805	2	T34212	Matches 595 NGGN-PTWTSWPCSTIGFQRQRSNSNTPRHHGRCVGQNREERYCNEHLLCPHMH 654
24	257	20.9	860	2	T16892	Qy 3 HGGFSQWSAWRACSYTCKGKIQKBSRLCNQPIJANGKPCQGSDELMRNC-QNKPCPYDG 61
25	242.5	19.7	951	2	T00260	Qy 62 SWSEKSLWEBCTRSGRGNQTRFTCNPSVQHGRPCBEGNAVEIIMNIRCPD-----115
26	23.5	19.3	254	2	T15952	Db 655 FWTGNGPWERCTAQGGI0ARRICEN-----GPDCAGCNVEYQSNTNPQCBLLKTT 708
27	23.5	19.1	919	2	T32241	Qy 116 -----115
28	23.5	19.1	947	1	B44294	Db 709 PWTPPTPVNISDNGDHYEPRYICKARLADPNILEVRQRIEMRYCSDGTGCGSTGCL 768
29	231.5	18.8	1558	2	C89114	Qy 116 -----VH GAWSAWQPGTCSSESCGKGQTQTRARLCNNPPAFCGGGARQRTGCGSDVVPQY 208
						Db 829 BYECNTLPCPVDWSCMSPWTKSCATGGHMYRTRCSNPAVY 875

RESULT 2
T00026

brain-specific angiogenesis inhibitor 1 - human	QY	124 QPWFCTSGKGTQTRARLICNNPPARGSYCDGAETQMQVCNERNCPHKGWATWAW 183		
A;Alternate name: BAII protein	Db	407 SSWSQSVTSVNGTQQRSTC - AAANGSECRGPWAESRECYNPECTANGQWNQHW 464		
C;Species: Homo sapiens (man)				
C;Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 09-Jul-2004				
R;Nishimori, H.; Shiratsuchi, T.; Urano, T.; Kiyono, Y.; Kiyono, K.; Yoshida submitted to the EMBL Data Library, June 1997	QY	184 SACSYSCGGGARQRTGCSDPV 205		
A;Reference number: Z14064	Db	465 SGCSKSDGGSWERRTTCQGAV 486		
A;Accession: 100026				
A;Status: translated from GB/EMBL/DDBJ				
A;Molecule type: mRNA				
A;Residues: 1-1584 <NIS>				
A;Cross-references: UNIPROT:O14514; EMBL:AB005297; NID:di175078; PID:di024528				
A;Experimental source: brain				
C;Genetics:				
A;Gene: GDB:BAI1				
A;Cross-references: GDB:9838088; OMIM:602682				
A;Map position: 8q4-8q4				
F;408-462/Domain: thrombospondin type 1 repeat homology <THR3>				
Query Match	42.2%	Score 519.5; DB 2; Length 1584;		
Best Local Similarity	45.8%	Pred. No. 2.2e-31; Indels 11; Gaps 5;		
Matches 92; Conservative 25; Mismatches 73;				
QY	8 QWSAQRACSTCGGIGQSRSLRCLNQPLPANGGRCQGDLEMRNCQKP-CPYDGSWEW 66			
Db	359 EWSPKPSVCSSTCGBSWOTRPF---VSSSYSTQCSPFLREQLCNNSAVCEVHGDAEW 415			
QY	67 SLWEBCTRSGRGNOTRTRCNBNPSVQHGGRCPEGNAVEBIMENIRPP--VRGAWSAW 123			
Db	416 SPWLCSSTSGRGRDRTRCPRP---QFQGSPCPEKTFNIALCPGRADVGDGHNEW 473			
QY	124 QPWFCTSGKGTQTRARLICNNPPARGSYCDGAETQMQVCNERNCPHKGWATWAW 183			
Db	474 SSWSQSVTSVNGTQQRSTC - AAANGSECRGPWAESRECYNPECTANGQWNQHW 531			
QY	184 SACSYSCGGGARQRTGCSDPV 204			
Db	532 GCSVTAGGSQRRERVCSQSP 552			
RESULT 3				
T00126 hypothetical protein KIAA0550 - human	QY	124 QPWFCTSGKGTQTRARLICNNPPARGSYCDGAETQMQVCNERNCPHKGWATWAW 183		
A;Cross-references: EMBL:AB01122; NID:g3043623; PID:93043624	Db	407 SSWSQSVTSVNGTQQRSTC - AAANGSECRGPWAESRECYNPECTANGQWNQHW 464		
A;Experimental source: brain				
C;Genetics:				
A;Note: KIAA0550				
C;Accession: 100326				
F;314-398/Domain: thrombospondin type 1 repeat homology <THR3>				
Query Match	40.9%	Score 501.5; DB 2; Length 984;		
Best Local Similarity	46.0%	Pred. No. 2.4e-30; Indels 9; Gaps 4;		
Matches 93; Conservative 15; Mismatches 85;				
QY	5 GFSQWSAQRACSTCGGIGQSRSLRCLNQPLPANGGKPCQGDLEMRNCQKP-CPYDGSW 63			
Db	293 GWEENSQWSTCQGGSQVRITCVSY--GTHESGPLRESRVCNNTALCPVHGSW 348			
QY	64 SEWSWIEBCTRSGRGNOTRTRCNNPSPYQHGGRCPEGNAVEIMCNTRPCVHGSW 123			
Db	349 EWSPWNLCSFTCGQRTRSTC - QYGGRPCGEPEHHKPCNIALCPVDQWQEW 406			
RESULT 5				
A40558 thrombospondin 1 precursor - mouse	QY	124 QPWFCTSGKGTQTRARLICNNPPARGSYCDGAETQMQVCNERNCPHKGWATWAW 183		
C;Species: Mus musculus (house mouse)	Db	407 SSWSQSVTSVNGTQQRSTC - AAANGSECRGPWAESRECYNPECTANGQWNQHW 464		
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 15-Mar-2004				
R;Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.				
DNA Res. 5, 31-39, 1998				
A;Title: Prediction of the coding sequences of unidentified human genes. IX. The completed genome sequence of human chromosome 22				
A;Reference number: Z14986; MUID:98290545; PMID:9628581				
A;Accession: 100326				
A;Status: preliminary; translated from GB/EMBL/DDBJ				
A;Molecule type: mRNA				
A;Residues: 1-984 <NAG>				
A;Cross-references: UNIPROT:AB01122; NID:g3043623; PID:93043624				
A;Experimental source: brain				
C;Genetics:				
A;Note: KIAA0550				
C;Accession: 100326				
F;314-398/Domain: thrombospondin type 1 repeat homology <THR3>				
Query Match	40.9%	Score 501.5; DB 2; Length 984;		
Best Local Similarity	46.0%	Pred. No. 2.4e-30; Indels 9; Gaps 4;		
Matches 93; Conservative 15; Mismatches 85;				
QY	5 GFSQWSAQRACSTCGGIGQSRSLRCLNQPLPANGGKPCQGDLEMRNCQKP-CPYDGSW 63			
Db	293 GWEENSQWSTCQGGSQVRITCVSY--GTHESGPLRESRVCNNTALCPVHGSW 348			
QY	64 SEWSWIEBCTRSGRGNOTRTRCNNPSPYQHGGRCPEGNAVEIMCNTRPCVHGSW 123			
Db	349 EWSPWNLCSFTCGQRTRSTC - QYGGRPCGEPEHHKPCNIALCPVDQWQEW 406			

A;Accession: A37905
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-490 <B0R>
A;Cross-references: GB:J05605; GB:J05606; NID:9201991; PIDN:AAA40431.1; PMID:9554390
R;Laherty, C.D.; O'Rourke, K.; Wolf, F.W.; Katz, R.; Seldin, M.F.; Dixit, V.M.
J. Biol. Chem., 267, 3274-3281, 1992
A;Title: Characterization of mouse thrombospondin 2 sequence and expression during cell
A;Reference number: A42587; PMID:1371115
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-1152; 'P'; 1154-1170 <LAH>
A;Cross-references: GB:M87276
A;Note: Sequence extracted from NCBI backbone (NCBIP: 81501)
R;Chen, H.; Neschlimann, D.; Nowlen, J.; Mosher, D.F.
FEBS Lett., 387, 36-41, 1996
A;Title: Expression and initial characterization of recombinant mouse thrombospondin 1
A;Reference number: S66787; MUID:96234006; PMID:8654563
A;Accession: S66787
A;Residues: 1-26,'X',28-37 <CHE>
A;Complex: homotrimer, disulfide linked
C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology;
C;Keywords: calcium binding, Glycoprotein, homotrimer
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-1170/Domain: von Willebrand factor type C repeat homology <VWF>
F;378-429/Domain: thrombospondin type 1 repeat homology <THRS>
F;434-490/Domain: thrombospondin type 1 repeat homology <THRS>
F;491-547/Domain: thrombospondin type 1 repeat homology <THRS>
F;551-586/Domain: EGF homology <EGF>
F;248, 360, 708, 1067/Binding site: carbohydrate (Asn) (covalent) #status predicted
Qry 5 GFSQSAVRAFACSTTGKGLQKRSRLCNQPLPANGKPCQGSDEMRNCQNPKC---PVD 60
Db 381 GWSPEWNTSCATCGNGIQRGRSDC---SLNNRCEGSSVQTRTCHIQECDKRFKQD 435
Qry 61 GSNSEWLSWEETRSRGCRGNCQPRTRTCNNPSVQHGRPCGEAVAEIMCNIRPCPVHGAW 120
Db 436 GGSHWSPPSSCSVTCGIVITRLCNSPSPQMNQGCEGARETRACKEDACPINGWW 495
Qry 121 SAMWPWGTCSESCKGQTARLICNNPPAFGSGYCGAETOMQVNERNPIHG---- 175
Db 496 GPNSPWDICSVTCGGVQRSRSLCNNTPQFGKDCDCTVQNVCNKQDCPDGCLSNP 555
Qry 176 ----KWAIIW--ASW--SACSYSCGGGARQRTRGCS 203
Db 556 CPAGAKCTSYDPGSWKCGCPPGYSGNLQ---CKD 588

RESULT 7
TSUHPI thrombospondin 1 precursor - human
C;Species: Homo sapiens (man)
C;Date: 23-Aug-1987 #sequence revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: A26155; A31274; A30140; A25812; A05172; A42927
R;Lawler, J.; Hynes, R.O.
J. Cell Biol., 103, 1635-1648, 1986
A;Title: The structure of human thrombospondin, an adhesive glycoprotein with multiple c-
A;Reference number: A26155; MUID:87057617; PMID:2430973
A;Accession: A26155
A;Molecule type: mRNA
A;Residues: 1-1170 <LAH>
A;Cross-references: UNIPROT:P07996; GB:X04665; NID:931737; PIDN:CAA28370.1; PID:937138
A;Note: parts of this sequence, including the amino end of the mature protein, were determined
R;Laherty, C.D.; Gierman, T.M.; Dixit, V.M.
J. Biol. Chem., 264, 11222-11227, 1989
A;Title: Characterization of the promoter region of the human thrombospondin gene. DNA sequence
A;Accession: A34274
A;Molecule type: DNA
A;Residues: 1-166 <LAH>
A;Cross-references: GB:J04835
R;Hennessy, S.W.; Frazier, B.A.; Kim, D.D.; Deckwerth, T.L.; Baumgartel, D.M.; Rotwein, P.
J. Cell Biol., 108, 729-736, 1989
A;Title: Complete thrombospondin mRNA sequence includes potential regulatory sites in the
A;Reference number: A30140; MUID:8913990; PMID:2918029
A;Accession: A30140
A;Molecule type: mRNA
A;Residues: 1-83,'A',85-522,'A',524-1170 <HEN>
A;Cross-references: EMBL:XI4787; NID:937464; PIDN:CAA32889.1; PID:937465
A;Note: parts of this sequence, including the amino end of the mature protein, were determined
R;Kobayashi, S.; Eden-McCutchan, F.; Fransom, P.; Bornstein, P.
Biochemistry 25, 8418-8425, 1986
A;Title: Partial amino acid sequence of human thrombospondin as determined by analysis of
A;Accession number: A25812; MUID:87157592; PMID:3030396
A;Accession: A25812
A;Molecule type: mRNA
A;Residues: 1-83,'A',85-397 <KOB>
A;Cross-references: GB:M25631; NID:9538353; PIDN:AAA36741.1; PID:9538354
R;Dixit, V.M.; Hennessy, S.W.; Grant, G.A.; Rotwein, P.; Frazier, W.A.
Proc. Natl. Acad. Sci. U.S.A., 83, 5449-5453, 1986
A;Accession: A05172
A;Molecule type: mRNA
A;Residues: 1-83,'A',85-374, 'RC' <DIX>
A;Cross-references: GB:XI4326; NID:9340005; PIDN:AAA61237.1; PMID:95533801
A;Note: parts of this sequence, including the amino end of the mature protein, were determined
A;Experimental source: brain
C;Genetics:

RESULT 6
T0027 brain-specific angiogenesis inhibitor 2 - human
R;Shiratsuchi, T.; Nishimori, H.; Ichise, H.; Nakamura, Y.; Tokino, T.
Cyogenet. Cell Genet. 79, 103-108, 1997
A;Title: Cloning and characterization of BAI2 and BAI3, novel genes homologous to brain-
A;Reference number: Z14066; MUID:98194217; PMID:9533023
A;Status: translated from GB/EMBL/DDJB
A;Molecule type: mRNA
A;Residues: 1-1572 <SH1>
A;Cross-references: UNIPROT:O60241; EMBL:AB005298; NID:93021698; PIDN:BA225362.1; PMID:930005
A;Accession: T0027
A;Cross-references: GB:XI4326; NID:9340005; PIDN:AAA61237.1; PMID:95533801
A;Note: parts of this sequence, including the amino end of the mature protein, were determined

C;Superfamily: human propeptidin precursor; thrombospondin type 1 repeat homology	
C;Keywords: complement alternate pathway; glycoprotein; homodimer; homotetramer; homotrimer	
F;5-97/Domain: thrombospondin type 1 repeat homology <THR1>	
F;104-160/Domain: thrombospondin type 1 repeat homology <THR2>	
F;161-224/Domain: thrombospondin type 1 repeat homology <THR3>	
F;225-282/Domain: thrombospondin type 1 repeat homology <THR4>	
F;283-345/Domain: thrombospondin type 1 repeat homology <THR5>	
F;446-468/Domain: thrombospondin type 1 repeat homology <THR6>	
P;32,55,108,111,114,165,229,232,350,353,356/Modified site: 2'-mannosyl-triptose	
P;366,396/Binding site: carbohydrate (Asn) (covalent) #status Predicted	
Query Match Score 38.5%; Best Local Similarity 40.7%; Pred. No. 1.e-28; Mismatches 88; Conservative 30; Indels 17; Gaps 8; Matches 88; #text_change 09-Jul-2004	
QY 4 GGFSQWSAARRACSVTGGKGIGKRSRLCNQPLPANGKPCQGSDLEMRNCQ-NFPCPVPGDS 62	
Db 106 GGNSBWPWGPGCSCVTSCKGTQIQRVCNDPAPKCGGH-CPGEAQQSQRCDTQXTCPHGA 164	
QY 63 WSEWSLWEECTRSRGGRNQ---TRTRCNPNPSVQH-GGRPCBEGNAVEIIIMCN-NIRPCP 115	
Db 165 WASGPWSPRSRSGSLGGQEPKRTSRSCSAPASHQPPGKPSGPAVEHKACSGLPPCP 224	
QY 116 VHGAWSARQPMGTCSESCKGKGICQTARLICNNMPFAFGGSYCDGAETQMQVCNER-NCPTH 174	
Db 225 VAGCNGPNSPLSPCSVTCGQTLERQTCGDTHPAIPRGSGFCADATRAQMCMNEAVPCPVN 284	
QY 175 GRATAWHSMSAC---SVSCGG--GARQRTQCSD 203	
Db 285 GENEAWGKMSDCSRLRMINSCTPGQOSRSRSRCGD 320	
RESULT 9	
T18856 angiogenesis inhibitor homolog - Caenorhabditis elegans	
C;Species: Caenorhabditis elegans	
C;Accession: T18856; T24653	
R;McMurray, A.	
A;Reference number: Z19031	
A;Accession: T18856	
A;Molecule type: DNA	
A;Cross-references: UNIPROT:Q8MYA8; EMBL:Z50004; PIDN:CAA90293.1; GSPDB:GN00028; CESP:CO:	
A;Experimental source: Clone C02B4	
R;McMurray, A.	
A;Reference number: Z19917	
A;Accession: T24653	
A;Status: preliminary; translated from GB/EMBL/DDJB	
A;Cross-references: <WIL>	
A;Experimental source: clone T07C5	
A;Genetics: C02B4.1	
A;Map Position: X	
A;Introns: 25/3; 70/3; 96/3; 139/3; 187/1; 234/2; 282/3; 376/2; 422/2; 478/3; 509/3; 566/	
Query Match Score 38.3%; Best Local Similarity 41.7%; Pred. No. 7.4e-28; Mismatches 88; Conservative 25; Indels 12; Gaps 7; Matches 88; #text_change 07-Sep-1990	
QY 4 GGFSQWSAARRACSVTGGKGIGKRSRLCNQPLPANGKPCQGSDLEMRNC-QNPKC---P 58	
Db 1187 GGSSLSWSSWSSCSDGGTGHQLRNRMSEPFNSNRYGCGNOTRTRCNPSVQHGRPCBEGNAVEIIIMCNIRPCPVH- 1246	
QY 59 VDSSWSERSLWEECTRSGRGNOTRTRCNPSVQHGRPCBEGNAVEIIIMCNIRPCPVH- 117	
Db 1247 VDGCGWTDMNTAWSCTCGRNGHRSRTECANPKPSOGQAQTCGSDFLNPSC-FDPARCHL 1305	
RESULT 8	
S00478 propeptidin - mouse (fragment)	
C;Species: Mus musculus (house mouse)	
C;Date: 07-SEP-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004	
C;Accession: S05478	
A;Title: Propeptidin, the terminal complement components, thrombospondin and the circumspace	
A;Reference number: S05478; PMID:3045564	
A;Accession: S05478	
A;Molecule type: mRNA	
A;Cross-references: UNIPROT:P11680; EMBL:X12905; NID:953786; PIDN:CAA31389.1; PID:953787	
C;Complex: a mixture of homodimers, homotrimers and homotetramers	
C;Function:	
A;Description: protects C3 convertase (C3bBb) from rapid inactivation	
A;Pathway: complement alternative pathway	

RESULT 10

Qy 118 -GAWAQPGTCSSESCGGTGTQTRARLNCNPPAEGGSYCDGAETOMQVCNERNC--PII 173
Db 1306 RDGGWTSWDTPCSAASCSSPPEK-GQQSGSLAHQTSLCDLPACDHE5 1364

A; Cross-references: GB:M81339
A; Experimental source: fibroblast
A; Note: sequence extracted from NCBI backbone (NCBIN:95091, MCBIP:95096)

C; Genetics:

A; Gene: GDB:TRBS2; TSP2
A; Cross-references: GDB:128789; OMIM:188061
A; MAD Position: 6927-6927
C; Complex: homotrimer, disulfide linked

C; Function:

A; Description: participates in cell migration and adhesion, and in platelet aggregation
C; Superfamily: thrombospondin 1: EGF homology; thrombospondin type 1 repeat homology; von Willebrand factor type C repeat homology; calcium binding; cell adhesion; glycoprotein; trimer
C; Keywords: beca-hydroxyasparagine; calcium-binding; signal sequence #status predicted >SIG>
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C; Accession: A33804
R; Lawler, J.; Duquette, M.; Ferro, P.
J. Biol. Chem. 266, 8039-1043, 1991.
A; Title: Cloning and sequencing of chicken thrombospondin.
A; Reference number: A39804; MUID:91217026; PMID:2022631
A; Accession: A33804
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-178 <RAW>
A; Cross-references: UNIPROT:P35440; GB:M60853; PID:9212763; PID:AAA51437_1; PID:912174
C; Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; von Willebrand factor type C repeat homology <WVC>
P; 325-383 Domain: von Willebrand factor type C repeat homology <WVC>
P; 386-437 Domain: thrombospondin type 1 repeat homology <TR1>
P; 442-487 Domain: thrombospondin type 1 repeat homology <TR2>
P; 499-555 Domain: thrombospondin type 1 repeat homology <TR3>
P; 658-697 Domain: EGF homology <EGF>

Query Match Score 466; DB 1; Length 1178;
Best Local Similarity 43.9%; Pred. No. 1.8e-27;
Matches 87; Conservative 19; Mismatches 76; Indels 16; Gaps 3;

Qy 5 GFSQWSANPACSVTCGKGIQKRSRLCNQPLPANGKPCQGSDLEMRCQNQKPCPV----D 60
Db 383 GWSWAENTQCSVTMCGSGTQGRSRSCDVTT----SNTLGPSIQTRACTSLSKCDTRRQD 437

Query Match Score 453; DB 1; Length 1172;
Best Local Similarity 40.4%; Pred. No. 1.6e-26;
Matches 80; Conservative 26; Mismatches 76; Indels 16; Gaps 3;

Qy 5 GFSQWSANPACSVTCGKGIQKRSRLCNQPLPANGKPCQGSDLEMRCQNQKPCPV----D 60
Db 383 GWSWAENTQCSVTMCGSGTQGRSRSCDVTT----SNTLGPSIQTRACTSLSKCDTRRQD 437

Query Match Score 446; DB 1; Length 1178;
Best Local Similarity 43.9%; Pred. No. 1.8e-27;
Matches 87; Conservative 19; Mismatches 76; Indels 16; Gaps 3;

Qy 5 GFSQWSANPACSVTCGKGIQKRSRLCNQPLPANGKPCQGSDLEMRCQNQKPCPV----D 60
Db 389 GWSWAENTQCSVTMCGSGTQGRSRSCDVTT----CTGHIQTRMCSPFKCDHRIRQD 443

Query Match Score 444; DB 1; Length 1178;
Best Local Similarity 43.9%; Pred. No. 1.8e-27;
Matches 87; Conservative 19; Mismatches 76; Indels 16; Gaps 3;

Qy 61 GWSWEWSLWEETCRSCSGRNQTRTRCNPPSYQHGGPRCEGNNAVEETIMCNIRCPVHGAW 120
Db 444 GGSHWNWPSWSSCVTCVGNTIRLNGNPPQMGGRNCVNGNGRETEKECAEAPCPVNGGW 503

Query Match Score 444; DB 1; Length 1178;
Best Local Similarity 43.9%; Pred. No. 1.8e-27;
Matches 87; Conservative 19; Mismatches 76; Indels 16; Gaps 3;

Qy 121 SAMQPGTCSSESCGGTGTQTRARLNCNPPAEGGSYCDGAETOMQVCNERNCPIHG--- 175
Db 504 GPWPSPWACTVTCGGGERTRVNSPEPOYGGKACVDQRMCNKRSCPVDGCLSNP 557

Query Match Score 444; DB 1; Length 1178;
Best Local Similarity 43.9%; Pred. No. 1.8e-27;
Matches 87; Conservative 19; Mismatches 76; Indels 16; Gaps 3;

Qy 176 --KWAATWSAACSVSCG 191
Db 564 CFPGAECNSYPDGWSWCG 581

RESULT 12

A42587

thrombospondin 2 precursor - mouse
Species: Mus musculus ('house mouse')
C; Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C; Accession: A42587; A39851
R; Liberty, C.D.; O'Rourke, K.; Wolf, F.W.; Katz, R.; Seldin, M.F.; Dixit, V.M.

A; Title: Characterization of mouse thrombospondin 2 sequence and expression during cell cycle
A; Reference number: A42587; MUID:92147683; PMID:1371115
A; Accession: A42587
A; Status: preliminary; not compared with conceptual translation
A; Molecule type: nucleic acid
A; Residues: 1-1172 <LAH>
A; Cross-references: UNIPROT:Q03350; GB:L07803; GB:M87275; NID:9340421; PID:NIA53064_1;
R; Lawler, T.L.; Milewicz, D.J.; Distech, C.M.; Byers, P.H.
A; Reference number: A47379
A; Molecule type: mRNA
A; Residues: 1-1172 <LAB>
A; Cross-references: UNIPROT:P35442; GB:LI12350; NID:9307505; PID:AAA03703_1; PID:9307506
A; Reference number: A47379
A; Molecule type: mRNA
A; Residues: 1-1172 <LAB>
A; Cross-references: UNIPROT:Q03350; GB:L07803; GB:M87275; NID:9340421; PID:NIA53064_1;
R; Lawler, T.L.; Milewicz, D.J.; Distech, C.M.; Byers, P.H.
A; Title: Thrombospondin II: partial cDNA sequence, chromosome location, and expression in human fibroblasts
A; Reference number: A42173; MUID:92217961; PMID:1555964
A; Molecule type: mRNA
A; Residues: 560-1172 <LA2>

Query Match 36.7%; Score 451.5; DB 2; Length 1172;
Best Local Similarity 39.5%; **Pred.** No. 2.1e-26; **Indels** 23; **Gaps** 6;
Matches 85; **Conservative** 27; **Mismatches** 80; **Avg. GC%** 45.5;

```

Qy      5  GFSOWSAMWACSVTCGKGKQRRSLRCLNQPLANGKRCQGSILEMENCNQNRPCKPV---D 60
Db     383  GWSWAENTBCSVCIGSGTQRERSCDVT----SNTCLGPBIQTCTSLGKCDTRIQN 437
Qy      61  GSWSWSLWBECTRSGRGNQTRTRTCNNPSYQHGRPCBEGNAVEIMCNLRCPVHGAW 120
Db     438  GGSHSHWSPSSCSYCUTCGVNTAQLRKLSPVQMGGRNCRCKSGREKXPQDPCKPDDGRW 497
Qy      121  SAVOPWGTCSESCGKGOTRTRLICNNPPAFCGSYCDGAETOMQCVNERNCPIHG---- 175
Db     498  SPNSPWSACTIVTAGGIRRSRCSNPPQGKDCVGDVTEHQMCNKRSCPIDGCLSNP 557
Qy      176  ---KWAATW--ASWSACSVSCGGAAQRTRGSD 203
Db     558  CFPGAKCNSFPDGSSWS-CG-SCPVGFGLNGTHCED 590

```

RESULT 13

properdin precursor [validated] - human

N; **Accessories:** factor P
C; Species: Homo sapiens (man)
C; Date: 17-Nov-2000 #sequence revision 17-Nov-2000 #text_change 09-Jul-2004
C; Accession: EMBL:X70818; PID:915679; PIID:CAA50220.1; PMID:935680
R; Nolan, K.F.; Kaluz, S.; Higgins, J.M.G.; Reid, K.B.M.
Biochem. J. 287: 291-297, 1992.
A; Title: Characterization of the human properdin gene.
A; Reference number: S29126; MUID:93038568; PMID:1417780
A; Accession: S29126
A; Molecule type: DNA
A; Residues: 1-469 <NOLL>
A; Cross references: UNIPROT:P27918; EMBL:X70818; PID:915679; PIID:CAA50220.1; PMID:935680

Eur. J. Immunol. 21, 771-776, 1991.
A; Title: Molecular cloning of the cDNA coding for properdin, a positive regulator of the complement system.
A; Reference number: S16150; MUID:91184288; PMID:2009915
A; Accession: S16150
A; Molecule type: mRNA
A; Residues: 1-456-'R' 458-469 <NOL2>
A; Cross references: EMBL:X57748
R; Reid, K.B.M.; Gagnon, J.
MoI. Immunol. 18, 949-959, 1981.
A; Reference number: A05319; MUID:82195224; PMID:7341961

A; Reference number: A05319
A; Molecule type: protein
A; Residues: 28-53 'O' 55-59 'G' 61 'I' 63;137-138 'P' 140-141 'P' 143-144 'X' 146-148 'Y'
A; Accession: T45112
A; Status: translated from GB/EMBL/DDJB
A; Molecule type: DNA
A; Cross references: EMBL:AB005165; PIDN:AAB61280.1
A; Experimental source: genomic DNA From individual with properdin deficiency type II
A; Accession: T45113
A; Status: translated from GB/EMBL/DDJB
A; Molecule type: DNA
A; Residues: 1-54 'X' 56-73 'X' 75-99 'W' 101-469 <WE1>
A; Accession: T45114
A; Status: annotated
A; Molecule type: DNA
A; Residues: 1-60 'X' 62-413 'D' 415-452 'XX' 455-469 <WE2>

A; Cross-references: EMBL:AF005666; PIDN:AC51626.1
A; Experimental source: genomic DNA from individual with properdin deficiency type III
R; Hartmann, S.; Hoistenga, J.
J. Biol. Chem. 275, 28569-28574, 2000.
A; Title: Properdin, the positive regulator of complement, is highly C-mannosylated.
A; Reference number: A55360; MUID:2045812; PMID:10878002
A; Contents: annotation
A; Note: identification and location of C-mannosylation sites by mass-spectroscopy
C; Genetics:
A; Gene: GDB:PPC
A; Cross-references: GDB:120275; OMIM:312060
A; Map position: Xp11.3-Xp11.23
A; Introns: 26/1; 76/2; 137/1; 102/1; 256/1; 314/1; 378/1; 415/2
C; Complex: a mixture of homodimers, homotimers and homoctetramers
C; Function: protects C3
A; Pathway: complement alternate pathway
C; Superfamily: human properdin precursor; thrombospondin type 1 repeat homolog
C; Keywords: complement alternate pathway; glycoprotein; homotetramer; homodimer; homotrim
F; 1-7/Domain: signal sequence #status predicted <SG>
F; 26-128/Domain: properdin #status experimental <PAT>
F; 76-128/Domain: thrombospondin type 1 repeat homology <THR1>
F; 15-19/Domain: thrombospondin type 1 repeat homology <THR2>
F; 19-255/Domain: thrombospondin type 1 repeat homology <THR3>
F; 26-31/Domain: thrombospondin type 1 repeat homology <THR4>
F; 314-377/Domain: thrombospondin type 1 repeat homology <THR5>
F; 378-440/Domain: thrombospondin type 1 repeat homology <THR6>
F; 428/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 36.5%; Score 449; DB 16; Length 469;
Best Local Similarity 40.1%; **Pred.** No. 1.6e-26; **Mismatches** 88; **Indels** 16; **Gaps** 7;
Matches 85; **Conservative** 23; **Score** 449; **DB** 16; **Length** 469;

```

Qy      4  GGFSQWSAWRACSVTCGKGOKRSRLCNQPLANGKPKCGSDLEMNCNQNP-CPVGDG 62
Db     137  GGWGWGPWPBCSVCSTGSTRTRRCHNPARKGGH-CPGQAQESSACDQQVCPTHA 195
Qy      63  WSEWSLWEECTRSOGRG---NQTRTRTCN-NPSVOHGRPCBEGNAVEIMC-NIRPCP 115
Db     196  WATGPWPWPCASCHGGPHEKTRSRKCSAPEPSQRPGKPGAYBQRRTCTGLPPCP 255
Qy      116  VHGWSANWQPWTGTCSESGKGQTOTRANICNNPPARFGSYCDGAETQMVCNNE-NCPH 174
Db     256  VAGMWGPWPVSQCPVTCGLQTMETQTCNHPQHSGPFCAQDAFRTHICNTAVCPVD 315
Qy      175  GKHTWAWWSAC-----SVSCEGGARQRTRG 200
Db     316  GENDSWGMSPCIRRNMSKISOCIEPGQSRG 347

```

RESULT 14

hypothetical protein F08C6.1 - *Caenorhabditis elegans*
C; Species: *Caenorhabditis elegans*
C; Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C; Accession: T15976
C; Description: Submitted to the EMBL Data Library, June 1995
A; Reference number: Z18440
A; Accession: T15976
A; Status: preliminary; translated from GB/EMBL/DDJB
A; Molecule type: DNA
A; Residues: 1-957 <BEN>
A; Cross-references: UNIPROT:Q19204; EMBL:U29378; PID:9868185; PID:g868184;
A; Accession: CESP:F08C6.1
A; Status: translated from strain Bristol N2
C; Genetics:
A; Gene: CESP:F08C6.1
A; Introns: 23/1; 135/3; 220/3; 285/3; 325/2; 376/3; 461/2; 498/3; 532/3; 627/2; 714/1; 7;
A; Status: translated from GB/EMBL/DDJB
A; Molecule type: DNA
A; Residues: 35.8% Score 441; DB 2; Length 957;
Query Match 35.8%; **Score** 441; **DB** 2; **Length** 957;
Best Local Similarity 35.9%; **Pred.** No. 1.1e-25;

Matches	85;	Conservative	22;	Mismatches	80;	Indels	50;	Gaps	5;
Qy	1 QVHGGFSQNSAWRACSYTCKGQIQLKRSRLCNP-----								LPANG 38
Db	657 RVGNENSTWTEBNHCSVGRGSQARYRKLNLSPIHTRLAFDGPGENKVNLIRTFKARS 716								
Qy	39 GKPC-----QGSDLEMRNQNKFDPDSWSENLSLWEECTRSOGRNQTPRT 86								
Db	717 YIMCSYRCNKLRKRNTISEKNEVRSCDNGPCNAIGWGTGWSCTSGPGTLVRQST 776								
Qy	87 CNNPSPVHGGPCEGNAAVEIMCNLRCPPEGAWSAWQPNGTCSESGKGTQTRALCN 146								
Db	777 CNR-----EPDGSAHEPRSCNATCQNDGIWSNEDSRYCGKURSRSC-- 827								
Qy	147 PPAFGGSSYCDGAETOMQVNERNCP1H--GRWATWASWACSVSGGGRQRTRGC 201								
Db	828 -----FQSGCMGASSEQQFCNEQACASSSANDWTGWSGSOCVSQCCAGTVRTRTC 879								

RESULT 15

T25061

hypothetical protein T21B6.3 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_change 09-Jul-2004

C;Accession: T25061

R,Cottage, A.

submitted to the EMBL Data Library, November 1995

A;Reference number: Z19975

A;Accession: T25061

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-788 <WLI>

A;Cross-references: UNIPROT:Q22631; EMBL:Z68011; PIDN:CAA92014.1; GSPDB:GN00028; CESP:T2

A;Experimental source: clone T21B6

C;Genetics:

A;Gene: CESP:T21B6.3

A;Map position: X

A;Intenzons: 20/1; 47/1; 76/1; 152/1; 735/2;

Query Match Similarity 33.9%; Score 417.5; DB 2; Length 788;

Best Local Similarity 39.0%; Prd. No. 5.3e-2; Matches 78; Conservative 20; Mismatches 79; Indels 23; Gaps 6;

Qy 2 VHGGFSQNSAWRACSYTCKGQIQLKRSRLCNP-----DEMRNCONKPCPVDG 61

Db 454 VSGVWHDDWS10SC1CGDKASRREEST-----NNCGGADVETEPNLGPQC-- 503

Qy 62 SWSEWSLWEECTRSGRNQTRTRTCNNPSVQEGGRPCGNAVEILMCNIRCPVGEAWS 121

Db 504 TWSSWCEVTSCTSASCGSQGRERTRFCH----LGTRNCEGHDFYESEFCSAFCP--EWS 555

Qy 122 AWQFWGTCSESSECGKGQTQTRARLNNPPAFFGSSYCDGAETOMQVNERNCP1HKGWATWA 181

Db 556 QWEWQGCVTCCGGVAVRQRTCLG--GFFGDHLQCGPKTEORACDGGPCSD--WSPWQ 610

Qy 182 SWSDCSVSGGGRQTRC 201

Db 611 EWSTCSASGSQMKRQVC 630

Search completed: November 17, 2004, 15:56:20
Job time : 45 secs



GenCore version 5.1.6
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OM protein - protein search, using sw model

Run On: November 17, 2004, 15:30:24 ; Search time 194 Seconds

(without alignments)
616.897 Million cell updates/sec

Title: US-10-019-065A-1

Perfect score: 1231

Sequence: 1 QVHGGESQWSANRACSVTCG.....SCGGGARQRTRGSDPYQY 208

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries

Database : UniProt 02:
1: uniprot_sprot:
2: uniprot_trembl:
*:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	1231	100.0	5636	Q96rw7	Q96rw7 homo sapien
2	1230	99.9	2673	Q96sc3	Q96sc3 homo sapien
3	533.5	43.3	1077	1	Q8CCM0 MOUSE
4	530.5	43.1	1582	2	Q8CCM0
5	528.5	42.9	1388	2	Q7qkd0 anophelis g
6	522.5	42.4	1074	1	Q13591 homo sapien
7	519.5	42.2	1584	1	BALI_HUMAN
8	511.5	41.6	1093	1	SM3B_HUMAN
9	511.5	41.6	1151	2	Q6D8S9
10	507.5	41.2	478	2	Q8BYT5
11	507.5	41.2	632	2	Q6ZPQ8
12	507.5	41.2	632	2	BAC98172
13	507.5	41.2	1093	1	SM5B_MOUSE
14	506.5	41.1	1088	2	Q6PCK8
15	506.5	41.1	1098	2	AAH59288
16	504.5	41.0	612	2	Q6Z9N6
17	504.5	41.0	612	2	BAC97972
18	504.5	41.0	1522	1	BAT3_MOUSE
19	503.5	40.9	1522	1	AAI13_HUMAN
20	500.5	40.7	Q6DCS2		
21	496.5	40.3	1549	2	O6PEN0
22	496.5	40.3	1549	2	AAH56926
23	492.5	40.0	1170	1	TSP1_BOVIN
24	492.5	40.0	1170	1	TSP1_MOUSE
25	492.5	40.0	1171	2	OBOTQ1
26	492.5	40.0	1171	2	QBCB2
27	492.5	40.0	1560	2	QBCBM1
28	490	39.8	1092	2	Q6UY12
29	489.5	39.8	1092	2	AAQ8491
30	489.5	39.8	1572	1	BAI2_HUMAN
31	489.5	39.8	1573	2	Q8NGW8

ALIGNMENTS

P07996	homo sapien	32	488.5	39.7	1170	1	TSP1_HUMAN
Q7LIS3	rattus norvegicus	33	486.5	39.5	1170	2	AAQ14549
AAQ14549	rattus norvegicus	34	486.5	39.5	1170	2	AAQ14549
Q7MT33	mus musculus	35	483	39.2	1122	2	Q7MT33
Q7MT33	mus musculus	36	474.5	38.5	1437	1	PROP_MOUSE
P2168	mus musculus	37	472.5	38.4	1173	1	TSP1_XENLA
P35448	xenopus laevis	38	472	38.3	1461	2	Q8NTA8
Q8NTA8	xenopus laevis	39	466	37.9	1178	1	TSP2_CHICK
P35448	gallus gallus	40	460.5	37.4	975	2	Q7Z291
Q7Z291	caenorhabditis elegans	41	460.5	37.4	1020	2	Q9204
Q9204	caenorhabditis elegans	42	460.5	37.4	1020	2	Q8TU50
Q8TU50	caenorhabditis elegans	43	445.5	36.8	1172	1	TSP2_HUMAN
P25442	homo sapien	44	451.5	36.7	1172	1	TSP2_MOUSE
P03350	mus musculus	45	451.5	36.7	1172	2	Q7WTM3

RESULT 1

Q96rw7	PRELIMINARY;	PRT;	5636 AA.
ID	Q96rw7;		
AC			
DT	01-DEC-2001 (TREMBREL_19, Created)		
DT	01-DEC-2001 (TREMBREL_19, Last sequence update)		
DT	01-MAR-2004 (TREMBREL_26, Last annotation update)		
DB	Hemolin.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butteleostomi;		
NCBI_TaxID	9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Treat J.;		
RL	Submitted (JDN-1999) to the EMBL/GenBank/DBJ databases...		
DR	HSSP; P07996; 1LSL		
DR	GO; GO:0005521; F:ATP binding; IFA; DR		
DR	GO; GO:0005021; F:vascular endothelial growth factor receptor; IEA; DR		
DR	InterPro; IPR00154; Ax _n hydroxy-S.		
DR	DR; GO:0005059; F:calcium ion binding; IEA; DR		
DR	InterPro; IPR008742; EGFR.		
DR	DR; GO:0006468; P:protein amino acid phosphorylation; IEA; DR		
DR	InterPro; IPR00181; EGFR-Ca.		
DR	InterPro; IPR06209; GFR-like.		
DR	InterPro; IPR06605; GFR-like.		
DR	InterPro; IPR000303; Grow_fac_recept.		
DR	InterPro; IPR07110; Ig-like.		
DR	InterPro; IPR003598; Ig_C2.		
DR	InterPro; IPR01692; PEP_CYS_acsite.		
DR	InterPro; IPR00884; TSP1.		
DR	InterPro; IPR00134; VEGFR.		
DR	InterPro; IPR002035; VWF_A.		
PFam	PF07645; EGF CA; 8.		
PFam	PF07474; G2F; 1.		
PFam	PF00047; Ig; 44.		
DR	PF00090; TSP1.		
PRINTS	PIR1832; VEGFRECEPTOR.		
DR	SMART; SM00179; EGF CA; 7.		
SMART	SM0408; IgS; 43.		
DR	SMART; SM00205; TSP1; 6.		
DR	SMART; SM00327; VWA; 1.		
DR	PROSITE; PS00010; ASX_HYDROXYL; 5.		
PROSITE	PS00468; CBCROPIN; UNKNOWN_1.		
DR	PROSITE; PS01186; EGF CA; 3.		
PROSITE	PS50026; EGF-3; 5.		
DR	PROSITE; PS01187; EGF CA; 6.		
PROSITE	PS00335; Ig_LIKE; 44.		
DR	PROSITE; PS00539; THITOL_PROTEASE_HIS; UNKNOWN_1.		
DR	PROSITE; PS50092; TSP1; 6.		
KW	EGF-Like domain.		
SEQUENCE	5636 AA; 613673 MW; F000B319CBD7BS2C CRC64;		

DR	InterPro; IPR000884; TSP1.		
DR	IPR008085; TSP_1.		
PFam	PF01437; PSI; 1.		
PFam	PF01403; Sema; 1.		
DR	PRINTS; PRO17075; TSPREPEAT.		
SMART	SM00423; PSI; 1.		
SMART	SM00630; Sema; 1.		
SMART	SM00209; TSP1; 6.		
PROSITE	PS51004; SEVA; 1.		
PROSITE	PS50092; TSP1; 6.		
KW	Developmental protein; Glycoprotein; Multigene family; Neurogenesis;		
KW	Repeat; Signal; Transmembrane.		
PT	SIGNAL	1	21
PT	CHAIN	22	1077
PT	DOMAIN	22	971
PT	TRANSMEM	972	992
PT	DOMAIN	993	1077
PT	DOMAIN	35	484
PT	DOMAIN	540	593
PT	DOMAIN	595	651
PT	CARBOHYD	653	702
PT	DOMAIN	707	765
PT	DOMAIN	784	839
PT	DOMAIN	841	896
PT	DOMAIN	897	944
PT	CARBOHYD	147	147
PT	CARBOHYD	168	168
PT	CARBOHYD	227	227
PT	CARBOHYD	277	277
PT	CARBOHYD	323	323
PT	CARBOHYD	367	367
PT	CARBOHYD	536	536
PT	CARBOHYD	591	591
PT	CARBOHYD	717	717
PT	CARBOHYD	933	933
SEQUENCE	1077 AA;	120826 MW;	EDABODDDAA42789F CRC64;
Query Match	Best Local Similarity	43.3%	Score 533.5; DB 1; Length 1077;
Matches 98;	Conservative	34.1%; Pred. No 2.7e-34;	DB 1;
Matches 98;	Mismatches	23; Gaps 79; Indels 87; Gaps 3;	
Qy	3 HGGFSQSWAARRASVTTCGKGIQKRSRLCNQPLPANGGKPCQGSDLEMRNC-ONKPCPVGD 61		
Db	595 NGGTGTPWTSWPSCTTCGGFQTRQRSSNPTRHGGRVCVQNREPPCNHLLCPHV 654		
Qy	62 SWSEWSLWEEPECTS CSGRNQTRPTCNCNPVQHGGRCPEGNAYEITMNCIRPCP-----	115	
Db	655 FWTGWGPWRCTAQGGGQARERTCEN-----GPDAGANVEYHPCNNTACPELKKT 708		
Qy	116 -----	115	
Db	709 PWTWTPVNWISDNCGGHYB0RFRTCKARLPDPNLLEYGRQIEMRYCSSDTSGCSTDGL 768		
Qy	116 -----	115	
Db	769 SGDPLRAGFYSANTHVGNSAWTWSQSRDCRGIRNRRVCNNPKFQGMPCLGSP 928		
Qy	162 QM0YCNCERNICPIFGKWAHNTWASWCASVSYGGARQRTGCSDFVPQY 208		
Db	829 EFQBCNLLPCPVdgWVSCMSSWSKCSATGGHMYMRTRCSNPAPY 875		
RESULT 4	Q8CGM0	PRELIMINARY;	PRT; 1582 AA.
ID	Q8CGM0	PRELIMINARY;	PRT; 1582 AA.
AC	Q8CGM0;	Created)	
DT	01-MAR-2003 (TREMBrel. 23,	Last sequence update)	
DT	01-MAR-2003 (TREMBrel. 23,	Last annotation update)	
DT	01-OCT-2003 (TREMBrel. 25,	Last annotation update)	
GN	Name=Baili.		
OS	Mus musculus (Mouse).		
RESULT 5	Q7QKD0	PRELIMINARY;	PRT; 1388 AA.
ID	Q7QKD0	PRELIMINARY;	PRT; 1388 AA.
AC	Q7QKD0;	Created)	
DT	01-MAR-2004 (TREMBrel. 26,	Last sequence update)	
DT	01-MAR-2004 (TREMBrel. 26,	Last annotation update)	
DB	AGCP14698 (Fragment).		

Name=agCCG49943; ORFNames=ENSANGG0000019365;
 GN Anopheles gambiae str. PEST.
 OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Anophelidae; Diptera; Nematocera; Culicoidea; Anophelidae.
 NCBI_TAXID=180454;
 [1] _
 RN SEQUENCE FROM N.A.
 RP STRAIN=PEST;
 RA Anopheles Genome Sequencing Consortium;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR AAC01008799; EAA03790_1; -.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008084; TSP_1.
 DR Pfam; PF00047; Ig; 6.
 DR Pfam; PF00090; TSP_1; 4.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR PROSITE; PS50335; Ig_LIKE; 9.
 DR PROSITE; PS50092; TSP1; 4.
 FT NON_TER 1388 1388 AA; 153015 MW; 3A054C8EF1900324 CRC64;
 SQ SEQUENCE 1388 AA; 153015 MW; 3A054C8EF1900324 CRC64;

Query Match Score 42.9%; Score 54.5%; DB 2; Length 1388;
 Best Local Similarity 42.2%; Pred. No. 8.6e-34; Gaps 3;
 Matches 89; Conservative 36; Mismatches 77; Indels 9; Gaps 3;

QY 6 FSOVSAWRACSVTGGKGIQRSSRUC--NQPLPANGK--PQQESDLIENRKQNPCKPVDGS 62
 Db 1072 WSPGAWAQSOSATCGSGIQRSSRUCLLVNGSPHGERFNCVENVELJKACEBLLPCPYNGG 1131
 Qy 63 WSEWLWERCTRSC-----GRGNQTRTRCNPSVOHGGRPCEGNAYEIMCNIRCPV 116
 Db 1132 WGEWTGWNSNCISLSCVSEPGVSRIRRSRACDKPAPSLGGKVCGVGEAYEEBCHVKYCP1 1191
 Qy 117 HGAWSAQOPWGTCSESCGGKGQTQTRALCNPAPPAGFSYYCGDAETQMOVCHERNCPDTHGK 176
 Db 1192 DGGTTAWSWTTGCBPCCGRSRMRSRQSSNPPVERHGGLPQCDGAESEVAKVQECHVDDG 1251
 Qy 177 WATWASWSRCSVSOGGGARQRTRGCSDEVPQ 207
 Db 1252 WSEWRWSPCNKSCGGKGITKRRRYCNCNNEPK 1282

RESULT 6

SMA-HUMAN STANDARD; PRT; 1074 AA.
 ID SMA-HUMAN ; STANDARD ;
 AC Q13591; O60408;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 01-OCT-2004 (Rel. 4, Last annotation update)
 DE Semaphorin 5A precursor (Semaphorin F) (Sema F).
 GN Name=SEMA5A; Synonyms=SEMAF;
 OS Homo sapiens (Human).
 OC Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Primates; Catarrhini; Hominidae; Homo.
 RN NCBI_TAXID=9606;

[1] _
 RN SEQUENCE FROM N.A.
 RP MEDLINE-9815554; PubMed=9464278;
 RA Simmonds A.D.; Puschel A.W.; McPherson J.D.; Overhauser J.; Lovett M.;
 RT "Molecular cloning and mapping of human semaphorin F from the Cri-du-
 chat candidate interval,"
 RT Biochem. Biophys. Res. Commun. 242:685-691 (1998).
 RL SBOQUENCE OF 1-494 FROM N.A.
 RP Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 PA Kalicki J.; Harman G.;
 CC _- FUNCTION: May act as positive axonal guidance cues.
 CC _- SUBCELLULAR LOCATION: Type I membrane protein.
 CC _- SIMILARITY: Belongs to the semaphorin family.

Query Match Score 42.4%; Score 522.5%; DB 1; Length 1074;
 Best Local Similarity 33.1%; Pred. No. 2e-33; Gaps 3;
 Matches 95; Conservative 24; Mismatches 81; Indels 87; Gaps 3;

Oy 3 HGGFSQNSAWRACSVTGGKGIQRSRLQNPPLANGKPCQSDLEMRC-QNKPCPVDG 61
 Db 595 NGGTWTPWNSWSPCSTTCCIGFQYRQRSCSNPTPRHGCRCVGQNBERYCNHEHLCPPH 654

Qy 62 SWNSWLWEECTRSGRGNQTRTCNNPSPVQHGGRCGNAVELIMCNIRPCP----- 115
 Db 655 FWTGWGPWRCAQGGG1QARRICEN-----GPDAGCNVEYOSCNTPCPPEKKRT 708
 Qy 116 ----- 115
 Db 709 PWTPWTPVNISDNGDHYEQRFRTYCKARLADPNLLEVGRQIEMRYCSDGTSGCSTDGL 768
 Qy 116 ----- VHGANASANOPKGTCSESFGKGFOTRAILCNCNPPAFEGSYCDGAET 161
 Db 769 SGDFLRAGRYSAHTVNGAWASANTWSWSQCSRDSSRGRLRNREVCNNPEPKCGMPCLGPSL 828
 Qy 162 QMOVYCNERNCNPPIHGKWAATWASACSVSCGGGARQRTGCSDPVPOY 208
 Db 829 EYEQCNTPCPDVGSWCSWPXTKCSATCGGSHMTRTSNSNPAY 875

RESULT 7
 BAI1_HUMAN STANDARD; PRT; 1584 AA.
 AC O145I4;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2004 (Rel. 44, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Brain-specific angiogenesis inhibitor 1 precursor.
 GN Name=BAI1;
 OS Homo sapiens (Human);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN NCBI_Taxid=9606;
 RN SEQUENCE FROM N.A.
 RC TISSUE=Fetal brain;
 RX MEDLINE=98054121; PubMed=3393972;
 RA Nishimori H., Shiratsuchi T., Urano T., Kimura Y., Kiyono K., Nakamura Y.,
 RA Tatsumi K., Yoshida S., Ono M., Kuwano M., Nakamura Y., Totoku T.;
 RT "A novel brain-specific p53-target gene, BAI1, containing
 RT thrombospondin type 1 repeats inhibits experimental angiogenesis."
 RL Oncogene 15:2145-2150 (1997).
 RN [2]
 RP INTERACTION WITH BAPI.
 RX MEDLINE=98321173; PubMed=9647739;
 RA Tokino T.; Futamura M., Oda K., Nishimori H., Nakamura Y.,
 RT "Cloning and characterization of BAI1-associated protein 1: a PDZ
 domain-containing protein that interacts with BAI1.";
 RL Biochem. Biophys. Res. Commun. 247:597-604 (1998).
 CC -!- FUNCTION: Likely to be a potent inhibitor of angiogenesis in brain
 CC and may play a significant role as a mediator of the p53 signal in
 CC suppression of glioblastoma. May function in cell adhesion and
 CC signal transduction in the brain.
 CC -!- SUBUNIT: Interacts with BAI1 and PHHIP.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Likely to be
 CC concentrated at cell-cell adhesion sites.
 CC -!- TISSUE SPECIFICITY: Specifically expressed in brain. Reduced or no
 CC expression is observed in some glioblastoma cell lines and cancer
 CC tissues.
 CC -!- INDUCTION: By p53.
 CC -!- DOMAIN: The TSP1 repeats inhibit in vivo angiogenesis in rat
 CC cornea induced by BPGF.
 CC -!- SIMILARITY: Belongs to family 2 of G-protein coupled receptors.
 CC -!- SIMILARITY: Contains 1 GPS domain.
 CC -!- SIMILARITY: Contains 5 TSP type-1 domains.
 CC

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 or send an email to license@isb-sib.ch).

Query Match	42.2%;	Score	519.5;	DB	1;	Length	1584;	
Best Local Similarity	45.8%;	Pred.	No. 5.1e-33;					
Matches	92;	Conservative	25;	Mismatches	73;	Indels	11;	Gaps
Qy	8	QWSAWRACSVTCKGKIQRSRLCNQPLDANGKPCQGSDLENRNCNKP-CPVDGSSWSEW	66					
Db	359	EWSFWVSVCSSTCGQWTRRF--VSSYSTQCSPRLBQLCNNSAVPVHGADEW	415					
Qy	67	SLWEETCRSQRSGRNQTRTRCNPSVOHGRPCEGNAVEIIMCNTRCP--VHGRSAW	123					
Db	416	SPMSLCSSTCGRFDRTRCP--QFGGNCEGPKQTFCNIALCPGRADVGDNNNEW	473					
Qy	124	QPGTCTCSBCKGKTQTRALCNPPAEGGSYCDGAETOMCVNCERNPPIGKWTASW	183					
Db	474	SSNSACASCSQRQRQRREVCNG--PSYGABCQGHNVETRUCFLQQCPVIGKWAWSW	531					
Qy	184	SACSVSCGGGARQRTGSDP	204					
Db	532	GSCSVTCAGSQRRERVCSGP	552					
RESULT 8								
ID	SM3B_HUMAN	STANDARD;	PRT;	1093	AA.			
AC	Q9283;							
DT	10-OCT-2003	(Rel. 42, Created)						
DT	10-OCT-2003	(Rel. 42, Last sequence update)						
DT	10-OCT-2004	(Rel. 45, Last annotation update)						
DE	Semaphorin 5B precursor.							
GN	Name=SEMA5B; Synonyms=KIAA1445;							
OS	Homo sapiens (Human).							
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;							
RN	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.							
OX	NCBI_TaxID=9606;							
RN	SEQUENCE FROM N.A.							
RC	TISSUE=Brain;							
RX	MEDLINE=0277482; PubMed=10819331;							
RA	Nagase T., Kikuno R., Ishikawa K.-I., Hirose M., Ohara O.							
RT	"Prediction of the coding sequences of unidentified human genes. XVII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro."							
PL	DNA Res 7:143-150(2000).							
CC	-!- FUNCTION: May act as positive axonal guidance cues (By							
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.							
CC	-!- SIMILARITY: Belongs to the semaphorin family.							
CC	-!- SIMILARITY: Contains 1 Sema domain.							
CC	-!- SIMILARITY: Contains 7 TSP type-1 domains.							
CC	-----							
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CC	-----							
DR	EMBL: AB040878; BAA95869-1; ALT_INIT.							
DR	Genev: HGNC:10737; SEMA5B							
DR	InterPro: IPR003659; Plexin-like.							
DR	InterPro: IPR001657; Semax_repeat.							
DR	InterPro: IPR00884; TSP1.							
DR	InterPro: IPR008085; TSP_1.							
DR	PFam: PF01437; Pst1.							
DR	PFam: PF01403; Sema_1.							
DR	PRINTS: PRO1705; TSP1_REPEAT.							
DR	SMART: SM00423; PSI_1.							
DR	SMART: SM00630; Sema_1.							
DR	SMART: SM00209; TSP1_5.							
DR	SEQUENCE FROM N.A.							
RC	SEQUENCE FROM Tissue.							
RESULTS	9							
Q6D89	PRELIMINARY;							
AC	Q6D89;	PRT;	1151	AA.				
DT	01-OCT-2004	(TREMBrel.	28	Created)				
DT	01-OCT-2004	(TREMBrel.	28	Last sequence update)				
DT	01-OCT-2004	(TREMBrel.	28	Last annotation update)				
DE	SEMA5B protein.							
GN	Name=SEMA5B;							
OS	Homo sapiens (Human).							
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.							
OX	[1]							
RN	SEQUENCE FROM Ovary;							
RC	TISSUE=Ovary.							

Qy	3 RGGPSQWAWRACSVTCGKIQKRSRLQNPQLPANGKPCCGSDLEMNC-QNKPCPVDG	Db	259 PWTPLPVNTVQGARQQRERFTCRAFLPDPHGLQFGKRRRTETRTPADGTGACDTDAL 318
Db	13 NGAWTAWSSAQCSNSTCGIGQVRQCSRGSNPPRHEGRICVKRSRERFCTNPPVPI	Qy	116 -----VHGAWSAWOPWGTSSESCRGKGTQTRARLNNPPAFGGSYCDGAET 161
Db	62 SWSEWSLWEBCTRSGRNQTRTRTCNNPSVQHGRPECBGNAVEITIMCNIRCP-----	Db	319 VEDLIRSSTSPTHLNGWATGPWSSSRDCELGFRVKTCTNPEBRNGGLPCVGDA 378
Qy	73 FWAWSGMSKCSNNCGGGVQSRRCEN----GNSCPGGVEFKTCNPACPEVRNT 126	Qy	162 QMOVNCNERNCPTICKWATWASVCSVCGGARQRTGCSDFVP 206
Db	116 -----	Db	379 EYQDCNPNQCPVRCAWSCTAWSQCSASCGGHHYQRTSCTSAP 423
Qy	127 PWTPLPVNTVQGARQQRERFTCRAFLPDPHGLQFGKRRRTETRTPADGTGACDTDAL 186	RESULT 12	
Qy	116 -----VHGAWSANOPWGTCSESCGKGQTTRARLNNPPAFGGSYCDGAET 161	ID	BAC98172 PRELIMINARY;
Db	187 VEDLIRSSTSPTHLNGWATGPWSSSRDCELGFRVKTCTNPEBRNGGLPCVGDA 246	ID	BAC98172/ PRELIMINARY;
Qy	162 QMOVNCNERNCPTICKWATWASVCSVCGGARQRTGCSDFVP 206	AC	BAC98172/ PRELIMINARY;
Db	247 EYQDCNPNQCPVRCAWSCTAWSQCSASCGGHHYQRTSCTSAP 291	DT	02-MAR-2004 (TREMBrel. 27, Created)
RESULT 11		DT	02-MAR-2004 (TREMBrel. 27, Last sequence update)
Q6ZQ8	PRELIMINARY;	DT	02-MAR-2004 (TREMBrel. 27, Last annotation update)
AC	Q6ZQ8; PRELIMINARY;	DT	02-MAR-2004 (TREMBrel. 27, Last annotation update)
DT	05-JUL-2004 (TREMBrel. 27, Created)	GN	MKTA1A145 Protein (Fragment).
DT	05-JUL-2004 (TREMBrel. 27, Last sequence update)	OC	Mus musculus (Mouse).
DE	MKTA1A145; protein (Fragment).	OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Name=mkTA1A145;		OC	Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.
GN		OC	
OS		NCBI_TaxID=10090;	
OC		RN	[1]
OC		RP	SEQUENCE FROM N_A.
OX		RC	SEQUENCE=Embryonic tail; Okuno R., Ohara R., Inamoto S., Koseki H., Hiraoaka S., Okazaki N., Kikuno R., Ohara O., Koga H.; Saga Y., Nagase T., Ohara O., Koga H.; "Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene: RT III. The Complete Nucleotide Sequences of 500 Mouse KIAA homologous cDNAs Identified by Screening of Terminal Sequences of cDNA Clones RT Randomly Sampled from Size-fractionated Libraries."; DNA Res 10:167-180(2003); DR EMBL; AKI29366; BAC98172.1; -.
RN		FT	NON_TER 1 69037 MW; 78CD7F28C3FFF3E7 CRC64;
FT		SQ	SEQUENCE 632 AA; 69037 MW; 78CD7F28C3FFF3E7 CRC64;
Query Match 41.2%; Score 507.5; DB 2; Length 632;			
Best Local Similarity 31.9%; Pred. No. 2e-32; Gaps 3;			
Matches 91; Conservative 26; Mismatches 81; Indels 87; Gaps 3;			
Qy 3 HGGFSQWAWRACSVTCGKIQKRSRLQNPQLPANGKPCCGSDLEMNC-QNKPCPVDG 61			
DR SEQUENCE FROM N_A.			
RC TISSUE=Embryonic tail; PubMed=14621395;			
RA Okuno R., Ohara R., Inamoto S., Koseki H., Hiraoaka S., Okazaki N., Kikuno R., Ohara O., Koga H.; Saga Y., Nagase T., Ohara O., Koga H.; "Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene: RT III. The complete nucleotide sequences of 500 mouse KIAA homologous cDNAs identified by screening of terminal sequences of cDNA clones randomly sampled from size-fractionated libraries."; DNA Res 10:167-180(2003); DR EMBL; AKI29366; BAC98172.1; -.			
DR InterPro: IPR003659; Plexin-like.			
DR InterPro: IPR000215; Plexin_repeat.			
DR InterPro: IPR000854; TSP1.			
DR InterPro: IPR000855; TSP1.			
DR Pfam: PR01437; PS1; 1.			
DR PRINTS; PR01705; TSP1_REPEAT.			
DR SMART; SM0023; TSP1; 1.			
DR PROSITE; PS550092; TSP1; 5.			
DR SEQUENCE 632 AA; 69037 MW; 78CD7F28C3FFF3E7 CRC64;			
Query Match 41.2%; Score 507.5; DB 2; Length 632;			
Best Local Similarity 31.9%; Pred. No. 2e-32; Gaps 3;			
Matches 91; Conservative 26; Mismatches 81; Indels 87; Gaps 3;			
Qy 3 HGGFSQWAWRACSVTCGKIQKRSRLQNPQLPANGKPCCGSDLEMNC-QNKPCPVDG 61			
DR SM5B MOUSE STANDARD; PRT; 1093 AA.			
DB 145 NGAWTAWSSAQCSNSTCGIGFOVQRQCSRGSNPARHGGTCIVGKSREERFCNTPCVPVI 204			
Qy 62 SWSEWSLWEBCTRSGRNQTRTRTCNNPSVQHGRPECBGNAVEITIMCNIRCP-----			
DB 205 FWAWSGMSKCSNNCGGGVQSRRCEN----GNSCPGGVEFKTCNPACPEVRNT 258			
Qy 145 NGAWTAWSSAQCSNSTCGIGFOVQRQCSRGSNPARHGGTCIVGKSREERFCNTPCVPVI 204			
DB 319 VEDLIRSSTSPTHLNGWATGPWSSSRDCELGFRVKTCTNPEBRNGGLPCVGDA 378			
Qy 162 QMOVNCNERNCPTICKWATWASVCSVCGGARQRTGCSDFVP 206			
DB 379 EYQDCNPNQCPVRCAWSCTAWSQCSASCGGHHYQRTSCTSAP 423			
Qy 116 -----VHGAWSAWOPWGTSSESCRGKGTQTRARLNNPPAFGGSYCDGAET 161			
DB 30-MAY-2000 (Rel. 39, Created)			
Qy 62 SWSEWSLWEBCTRSGRNQTRTRTCNNPSVQHGRPECBGNAVEITIMCNIRCP-----			
DB 01-OCT-2004 (Rel. 45, Last annotation update)			
DB Semaphorin 5B Precursor (Semaphorin G) (Sema G).			
Name=Sema5b; Synonyms=SEMAG, Semag;			
OS Mus: musculus (Mouse).			

